



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: REM/2D182C18

TO: James Schultz
Location: REM/2D182C18
Art Unit: 1635
Monday, March 01, 2004

Case Serial Number: 09/904568

From: Toby Port
Location: Biotech-Chem Library
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Phone: 571-272-2523

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Search Notes

Dear Examiner Schultz,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

- I am an examiner in Workgroup: Example: 1610
- Relevant prior art **found**, search results used as follows:
- 102 rejection
 - 103 rejection
 - Cited as being of interest.
 - Helped examiner better understand the invention.
 - Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- Foreign Patent(s)
- Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- Results verified the lack of relevant prior art (helped determine patentability).
- Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library, Remsen Bldg.



CC add the A7J epitope to the C-terminus of wild-type UbCH10 and its
 CC Cys114Ser mutant (see AAV31279). Tagged proteins were expressed in E.
 CC coli and used in tests to examine the in vivo and in vitro activity of
 CC UbCH10 and its dominant negative mutant
 XX SQ Sequence 48 BP; 9 A; 9 C; 17 G; 13 T; 0 U; 0 Other;
 Query Match 3.4%; Score 23; DB 2; Length 48;
 Best Local Similarity 83.9%; Pred. No. 5.1e+04; Pred. No. 5.6e+04;
 Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 304 CACCAACCTGAGCCTCACACTTCGGGAC 334
 Db 47 ACCAGGCCAGGCGCACCTACAGTAC 17

RESULT 2
 AAA35922/c
 ID AAA35922 standard; DNA; 36 BP.
 XX
 AC AAA35922;
 XX
 DT 26-JUL-2000 (first entry)
 DE Permutein linker encoding nucleotide sequence RGS152.
 XX
 KW Biologically-activated circularly-permuted protein; permutein; linker;
 KW permutein library generation; therapeutic property; antigen;
 KW immunotherapy; improve bio-distribution; half life; ss.
 XX
 OS Synthetic.
 XX
 PN WO200018905-A1.
 XX
 PD 06-APR-2000.
 XX
 PF 24-SEP-1999; 99WO-US020891.
 XX
 PR 25-SEP-1998; 98US3-0101908P.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 PT Lee SC;
 XX
 DR WPI; 2000-293145/25.

PT Preparation of biologically-activated circularly-permuted proteins by
 PT scanning permutedogenesis for generating libraries of permuteins with
 PT improved therapeutic properties.
 XX
 PS Claim 11; Page 44; 100pp; English.

CC The preparation of biologically-activated circularly-permuted proteins
 CC comprises the use of a method comprising making a series of
 CC (permutations) of circularly permuted genes. The circularly permuted genes are inserted into
 CC a display vector, where they are expressed so that the proteins they
 CC encode are presented on the surface of the display vector. A library of
 CC display vectors presenting the expressed circularly permuted proteins is
 generated. A target protein that can bind a biologically active
 CC circularly permuted protein can be used to affinity select the presenting
 CC display vectors. The selected display vectors can be isolated and
 analysed to identify the presented circularly permuted protein. The
 CC permuteins conform to the structure of a parent protein consisting of a
 segment derived from the carboxy portion of the parent protein, a segment
 derived from the amino terminus of the parent protein, and a linker or
 chemical bond linking the amino and carboxy terminal derived portions.
 CC Nucleic acid sequences AA3576-A5943 encode linkers used to create the
 CC permuteins of the invention. The method is used to generate libraries of
 CC permuteins with improved therapeutic properties compared to their parent
 molecules. Permutes with little or no activity may be used as antigens
 CC for producing antibodies which are used in immunology or immunotherapy as
 probes or intermediates used to construct other useful permuteins.
 CC Permuteins have improved biological and therapeutic properties compared

CC to their two individual components due to alterations in bio-distribution
 CC or half-life
 XX SQ Sequence 36 BP; 5 A; 15 C; 10 G; 6 T; 0 U; 0 Other;
 Query Match 3.3%; Score 22.4; DB 3; Length 36;
 Best Local Similarity 81.2%; Pred. No. 6.6e+04; Pred. No. 6.6e+04;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 425 GCCCAGCGCGAGGGGCTGGCTGCCCCATG 456
 Db 35 GCCTGGAGAGGGGCTGGCCCGCATAT 4

RESULT 3
 AAU3116
 ID AAU3116 standard; DNA; 43 BP.
 XX
 AC AAU3116;
 XX
 DT 02-SEP-1998 (first entry)
 DE H chain variable region from mouse anti-My-10 PCR primer 1.
 XX
 KW Mouse; anti-My-10; H chain variable region; L chain variable region;
 KW antibody; heavy; light; CD8; human CD34 antigen; Hybridoma; anti-CD34;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN JPI015489-A.
 XX
 PD 16-JUN-1998.
 XX
 PR 27-NOV-1996; 96JP-00331647.
 XX
 PR 27-NOV-1996; 96JP-00331647.
 XX
 PA (ASAHI) ASAHI KASEI KOGYO KK.
 PA (ASAHI) ASAHI MEDICAL CO LTD.
 XX
 DR WPI; 1998-391043/34.

PT Recombinant antibody against human CD34 - and nucleic acid encoding it,
 PT used for efficient production of the antibody.
 XX
 PS Example 4; Page 7; 15pp; Japanese.

XX The present invention describes a nucleic acid which encodes an anti-My-
 CC 10 antibody. The present sequence represents a PCR primer for the H chain
 CC variable region of the antibody. Also described is a method for the
 CC production of a recombinant antibody in which the above nucleic acid is
 CC used to produce an antibody which combines with human CD34 antigen by
 CC gene recombination. The anti-CD34 antibody gene is used to produce
 CC recombinant anti-CD34 antibodies efficiently, which can be used in
 pharmaceuticals
 XX SQ Sequence 43 BP; 8 A; 15 C; 16 G; 4 T; 0 U; 0 Other;
 Query Match 3.2%; Score 21.4; DB 2; Length 43;
 Best Local Similarity 71.8%; Pred. No. 1.2e+05; Pred. No. 1.2e+05;
 Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 OY 513 CCCTGAGCGAGCTCTCTATGAGCTAACGTTCTAG 551
 Db 5 CCAGGGCGatGCGGAGCTGAGCTGAGCTGAGCTGAGCTGAG 43

RESULT 4
 AAU44243
 ID AAU44243 standard; DNA; 43 BP.
 XX

AC AAZ44243;
 XX
 DT 31-MAR-2000 (first entry)
 XX
 DE Murine CD4/CD34 recognizing antibody primer 7.
 XX
 KW Cluster differentiation; cell separation; antibody; CD4; CD34; leukemia;
 KW hematopoietic; undifferentiated; lymphocyte; bone marrow transplantation;
 KW HIV infection; autoimmune disease; murine; primer; ss.
 XX
 OS Mus sp.
 XX
 PN WO9961629-A1.
 XX
 PD 02-DBC-1999.
 XX
 PP 24-MAY-1999; 99WO-JP002711.
 PR 25-MAY-1998; 98JP-00159957.
 PR 26-MAY-1998; 98JP-00163023.
 XX
 PA (ASAHI) ASAHI KASEI KOGYO KK.
 PA (ASAHI) ASAHI MEDICAL CO LTD.
 XX
 PI Ono M, Soka T, Morimoto I, Miyamura K;
 DR WPI; 2000-086720/07.
 PT Devices containing antibodies recognising CD4 or CD34 and their use for
 PT the separation of CD4 or CD34 positive cells.
 PS Example 21; Page 54; 11pp; Japanese.
 XX
 CC This invention describes a novel device (1) for separating cluster
 CC differentiation (CD)-positive cells using a recombinant (chimeric or
 CC single-chain) antibody recognising CD4 or CD34. The devices are useful for the
 CC separation of CD4 or CD34 positive cells, which is useful for the
 collection of hematopoietic undifferentiated cells, elimination of
 CC lymphocytes from cells to be used in bone marrow transplantation, the
 detection of leukemic cells and the production of medicinal compositions
 CC for the treatment of HIV infection and autoimmune diseases. AAZ44237-
 XX Z44246 represent primers used to illustrate the method of the invention.
 XX
 SQ Sequence 43 BP; 8 A; 15 C; 16 G; 4 T; 0 U; 0 Other;
 Query Match 3-2%; Score 21.4; DB 3; Length 43;
 Best Local Similarity 71.8%; Pred. No. 1.2e+05;
 Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 513 CCCTGCAGCGGAGCCCTGATGCAGCTGAACTTCAG 51
 Db 5 CCCAGCGGCCATGCCAGGTGCACTGAAGCTAG 43
 RESULT 5
 AAL28467
 ID AAL28467 standard; DNA; 50 BP.
 XX
 AC AAL28467;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #1675.
 XX
 KW immunosuppressive; immunostimulatory; anti-inflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angioprotein; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytokine; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX

OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US035498.
 PR 28-DEC-1999; 99US 0173419P.
 PR 27-DEC-2000; 2000US 00173419.
 XX
 PA (CURA) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 DR WPI; 2001-465210/50.
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PR autoimmune diseases and infections.
 XX
 PS Claim 1; Page 1859; 4143PP; English.
 XX
 CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinases, cytokines, interferons, interleukins, G-
 CC protein coupled receptors and thioesterases. The present sequence is one
 CC such oligonucleotide. The oligonucleotides and the peptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of the protein listed above.
 CC Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 XX
 SQ Sequence 50 BP; 9 A; 14 C; 22 G; 5 T; 0 U; 0 Other;
 Query Match 3-2%; Score 21.4; DB 4; Length 50;
 Best Local Similarity 66.0%; Pred. No. 1.2e+05;
 Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 QY 56 ACTGGCGAGTGAGTTCCTGGGGACCACTTCCTCCACAGGTGGC 102
 Db 2 AGGGGAGACTGGCATGGAGCCATGCGCCAGGTGG 48
 RESULT 6
 AAX19291/C
 ID AAX19291 standard; DNA; 44 BP.
 XX
 AC AAX19291;
 XX
 DT 17-MAY-1999 (first entry)
 XX
 DE Human granulocyte colony-stimulating factor antisense primer oligo 1.
 XX
 KW Human; granulocyte colony-stimulating factor; G-CSF; hg-CSF;
 KW haemopoiesis disorder; primer; ss.
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9853072-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 21-MAY-1998; 98WO-KR000125.

PR 22-MAY-1997; 97KR-00020054.

XX (KORE-) KORAE RES INST BIOSCIENCE & BIOTECHNOLOG.

PA (JEIL-) JEIL PHARM CO LTD.

XX PI Jun H, Choi B, Lee Y, Sohn M;

XX DR WPI; 1999-131691/11.

XX PT New human granulocyte colony-stimulating factor (hg-CSF) containing a peptide at the N-terminus - useful in the treatment of haematopoiesis disorders.

XX PS Example 1; Fig 1; 19pp; English.

The present invention describes the N-terminal peptide of human granulocyte colony-stimulating factor (hg-CSF). The present invention also describes: (1) recombinant plasmid PYHM-G-CSF containing the cDNA for the peptide; and (2) E. coli BL21 (pPYHM-G-CSF) (KCTC 0477BP) transformed with the plasmid. The plasmid and E. coli strain are used to produce high yields of highly purified hg-CSF which when refolded has comparable biological activity of G-CSF. hg-CSF is used to treat haemopoietic disorders. The method of producing hg-CSF is less time-consuming and, therefore, more economical than previous methods because the protein is expressed in high yields without the need for further processing steps. AAI19290 to AAI19315 represent primer used in the synthesis of hg-CSF from an example of the present invention

SQ Sequence 44 BP; 9 A; 10 C; 20 G; 5 T; 0 U; 0 Other;

CC Best Local Similarity 69.0%; Pred. No. 1.3e+05; Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 493 CACAGAGGCCAGCTGCTCTGAGCCAGGGCTGTGAT 534

Db 43 CTCACAGGGCTCGCCAGCTCTGAGCCAGGGCTGTGAT 2

RESULT 7 AAI364/C

ID AAI33664 standard; DNA; 50 BP.

AC AAI33664;

XX DT 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #6872.

Immuno-suppressive; immuno-stimulatory; anti-inflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.

XX OS Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PR 28-DEC-2000; 2000WO-US035498.

XX PR 28-DEC-1999; 99US-0173419P.

XX PR 27-DEC-2000; 2000US-00173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

DR WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer, PT autoimmune diseases and infections.

XX PS Claim 1; Page 3347; 4143pp; English.

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cyclochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney), leukaemia, diseases of the nervous system and an infection of pathogenic organisms.

XX Sequence 50 BP; 12 A; 15 C; 13 G; 10 T; 0 U; 0 Other;

CC Query Match 3.2%; Score 21.2; DB 4; Length 50;

CC Best Local Similarity 69.0%; Pred. No. 1.4e+05; Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 76 GGAGGCCAGCTCTCCAGAGCTGGAGCAATGGCCGGCT 117

Db 45 GGTGCAGCTCTCCAGACITGGGGCAGGACACGGT 5

RESULT 8

AAU33563 ID AAU33563 standard; DNA; 50 BP.

XX AC AAU33563;

XX DT 24-JAN-2002 (first entry)

XX DE Human SNP oligonucleotide #6771.

Immuno-suppressive; immuno-stimulatory; anti-inflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; nervous system disease; ss.

XX OS Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PR 28-DEC-2000; 2000WO-US035498.

XX PR 28-DBCC-1999; 99US-0173419P.

XX PR 27-DBCC-2000; 2000US-00173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX DR WPI; 2001-465210/50.

XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,

PT onco genes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.

XX
 PS
 XX

Claim 1; Page 3315; 4143pp; English.

CC The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, CC histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinases, cytokines, interferons, interleukins, G- CC protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above.

CC Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis and Graves' disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney), leukemia, diseases of the nervous system and an infection of pathogenic organisms

XX Sequence 50 BP; 7 A; 11 C; 23 G; 9 T; 0 U; 0 Other;

Query Match 3.1%; Score 20.8; DB 4; Length 50;

Best Local Similarity 70.0%; Pred. No. 1.7e-05; Matches 28; Conservat

CC 0; Mismatches 12; Indels 0; Gaps 0;

QY 73 CTGGGGGCCAGCTTCTCAAGAGGTGGAGCAATGGCC 112
 Db 7 CGTGCGGGCTAGGGTCCATAGCAGCAGCACTGGTC 46

RESULT 9
 ABZ49057/C
 ID ABZ49057 standard; DNA; 40 BP.

AC ABZ49057;

XX DT 26-JUN-2003 (first entry)

DE Human ALDH1L1/FTHFD gene polymorphic site, #5840.

KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 3;

KW polymorphic site; drug evaluation; drug screening; genotyping;

KW genetic profiling; therapeutic customisation; adverse reaction;

KW clinical trial; drug approval; ds.
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 PT variation replace(20..21,CCT)
 PT /*tag= a

PN WO200252044-A2.

XX PD 04-JUL-2002.

XX 27-DEC-2001; 2001WO-JP011592.

XX PR 27-DEC-2000; 2000JP-0039443.

PR 02-MAY-2001; 2001JP-0013256.

PR 27-AUG-2001; 2001JP-00256862.

XX PA (RIKE) RIKEN KK.

XX PI Nakamura Y, Sekine A, Iida A, Saito S;

XX DR WPI; 2002-583571/62.

XX PT Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment Protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme

PT nucleic acid.

XX
 PS
 XX

Claim 23; Page 180; 2785pp; English.

CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety.

CC Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy.

XX Sequence 40 BP; 6 A; 15 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 3.1%; Score 20.6; DB 6; Length 40;

Best Local Similarity 74.3%; Pred. No. 1.8e+05; Matches 26; Conservat

CC 0; Mismatches 9; Indels 0; Gaps 0;

QY 133 CAGGAGCGTCAGAAGTGTCTGAGTTCTGG 167
 Db 36 CACGAGCAGCTGGAGACTGGCTGATGTTGG 2

RESULT 10
 ABZ46527/C
 ID ABZ46527 standard; DNA; 40 BP.

AC ABZ46527;

XX DT 26-JUN-2003 (first entry)

DE Human ALDH1L1/FTHFD gene polymorphic site, #3311.

KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 3;

KW polymorphic site; drug evaluation; drug screening; genotyping;

KW genetic profiling; therapeutic customisation; adverse reaction;

KW clinical trial; drug approval; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

PT variation replace(20..21,CCT)

PT /*tag= a

PN WO200252044-A2.

XX PD 04-JUL-2002.

XX DE Human granulocyte colony-stimulating factor sense primer oligo 12.
 XX PF
 XX KW Human; granulocyte colony-stimulating factor; G-CSF; hG-CSF;
 PR KW haematopoiesis disorder; primer; ss.
 PR KW OS Synthetic.
 02-MAY-2001; 2001JP-00155256.
 XX OS Homo sapiens.
 PA (RIKE) RIKEN KK.
 XX PN WO9853072-A1.
 PT Nakamura Y, Sekine A, Iida A, Saito S;
 XX PD 26-NOV-1998.
 DR XX 21-MAY-1998; 98WO-KR000125.
 XX 22-MAY-1997; 97KRR-00020054.
 XX PT (KORE) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 PA (JELI) JELI PHARM CO LTD.
 XX PA Jun H, Choi B, Lee Y, Sohn M;
 XX DR 1999-131691/11.
 XX PT New human granulocyte colony-stimulating factor (hg-CSF) containing a peptide at the N-terminus - useful in the treatment of haematopoiesis disorders.
 PS Example 1; FIG 1; 19pp; English.
 XX The present invention describes the N-terminal peptide of human granulocyte colony-stimulating factor (hg-CSF). The present invention also describes: (1) recombinant plasmid pYHM-G-CSF containing the cDNA for the peptide; and (2) E. coli BL21 (pYHM-G-CSF) (KCTC 0477BP) transformed with the plasmid. The plasmid and E. coli strain are used to produce high yields of highly purified hg-CSF, which when refolded has comparable biological activity of G-CSF. hg-CSF is used to treat haematopoiesis disorders. The method of producing hg-CSF is less time-consuming and, therefore, more economical than previous methods because the protein is expressed in high yields without the need for further processing steps. AAX19290 to AAX19115 represent primer used in the synthesis of hg-CSF from an example of the present invention.
 XX SQ Sequence 41 BP; 4 A; 12 C; 13 G; 12 T; 0 U; 0 Other;
 XX Query Match 3.1%; Score 20.6; DB 2; Length 41;
 XX Best Local Similarity 74.3%; Fred. No. 1.8e+05;
 XX Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 XX QY 498 GTGCCCTGCCTCCGACCGAGGTCTG 512
 XX Db 2 GTGTCCTGGTGCTCCATCTGCAGACTTCCTG 36
 RESULT 12 AAF6438/C
 ID AAF6438 standard; DNA; 42 BP.
 XX AAC86438;
 XX DT 25-JUN-2001 (first entry)
 DB Primer 172del-R.
 XX PCR primer; male sterile plant; RNAase inhibitor; ss.
 XX OS Unidentified.
 XX DN WO200124616-A1.
 XX PD 12-APR-2001.
 XX PCR 12-SEP-2000; 2000WO-JP006222.
 XX
 RESULT 11 AAX19312
 ID AAX19312 standard; DNA; 41 BP.
 XX AC
 XX DT 17-MAY-1999 (first entry)

PR 30-SEP-1999; 99JP-00279307.

XX PA (NISB) JAPAN TOBACCO INC.

XX PT Hamada K, Nakakido F;

XX DR WPI; 2001-266212/27.

Disclosure: Page 14; 29pp; Japanese.
The present invention relates to a method for producing male sterile rice and maize by inserting RNase gene plants. The method comprises inserting a promoter fragment upstream of an RNase gene and a second promoter, upstream of an RNase inhibitor protein gene and inserting it into the plant genome. The method is useful for producing male sterile tobacco, lettuce and rapeseed plants, but preferably rice and maize. The present sequence is a PCR primer used in the method of the present invention.

Sequence 42 BP; 12 A; 11 C; 13 G; 6 T; 0 U; 0 Other;
Query Match 3.0%; Score 20; DB 4; Length 42;
Best Local Similarity 68.3%; Pred. No. 2.2e+05; Mismatches 13; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 482 GTAGCAATCTCACCGTGCCTGGTCGTCCTCCCTGAGCC 522
Db 42 GTAATTTTGCCCTATGGTGCTGCTGTGACTGCGGCC 2

RESULT 13

ID ABZ43217 standard; DNA; 41 BP.

ID ABZ43217; AC ABZ43217;

XX DT 26-JUN-2003 (first entry)

DE Human N-methyltransferase PEMT gene polymorphic site, #5485.

KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 17; polyomorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds. OS Homo sapiens.

PH Key Location/Qualifiers

FT variation replace(21,T)

FT /*tag= a /standard_name= "Single nucleotide polymorphism (SNP)"

PN WO200252044-A2.

XX PD 04-JUL-2002.

XX FP 27-DEC-2001; 2001WO-JP011592.

XX PR 27-DEC-2000; 2000JP-0039443.

XX PR 02-MAY-2001; 2001JP-00135256.

XX PR 27-AUG-2001; 2001JP-00256862.

PA (RIKE) RIKEN KK.

XX PI Nakamura Y, Sekine A, Iida A, Saito S;

XX DR WPI; 2002-583571/62.

Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme

PT nucleic acid.

XX PS Claim 23; Page 172; 2785PP; English.

XX CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety.

CC Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy.

Sequence 41 BP; 6 A; 15 C; 14 G; 6 T; 0 U; 0 Other;
Query Match 3.0%; Score 20; DB 6; Length 41;
Best Local Similarity 72.2%; Pred. No. 2.5e+05; Mismatches 10; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 339 TCCAGGAGCTCTGCATCCCCAAGAGCTGGTGGGG 374
Db 2 TCGAGGGCCCTGCACTCCCGCAGCCAGTCCTGG 37

RESULT 14

ID ABZ43362 standard; DNA; 41 BP.

ID ABZ43362;

XX DT 26-JUN-2003 (first entry)

DE Human N-methyltransferase PEMT gene polymorphic site, #146.

KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 17; polyomorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

PH Key Location/Qualifiers

FT variation replace(1,T)

FT /*tag= a /standard_name= "Single nucleotide polymorphism (SNP)"

PN WO200252044-A2.

XX PD 04-JUL-2002.

XX FP 27-DEC-2001; 2001WO-JP011592.

XX PR 27-DEC-2000; 2000JP-0039443.

XX PR 02-MAY-2001; 2001JP-00135256.

XX PR 27-AUG-2001; 2001JP-00256862.

PA (RIKE) RIKEN KK.

XX PI Nakamura Y, Sekine A, Iida A, Saito S;

XX DR WPI; 2002-583571/62.

04-JUL-2002.	XX	Human pigmentation trait-related PCR primer - SEQ ID No 121.
27-DEC-2001; 2001WO-JP011592.	XX	Human; single nucleotide polymorphism; SNP; melanocortin-1 receptor;
27-DEC-2000; 2000JP-00399443.	KW	single nucleotide polymorphism; MC1R; agouti signalling protein; ASIP; race;
02-MAY-2001; 2001JP-00135256.	KW	genetic pigmentation trait; MC1R; hair colour; eye colour; forensic tool; PCR; primer.
27-AUG-2001; 2001JP-00256862.	XX	hair colour; eye colour; forensic tool; PCR; primer.
(RIKE) RIKEN KK.	XX	Homo sapiens.
Nakamura Y, Sekine A, Iida A, Saito S;	XX	WO200291047-A2.
WPI; 2002-583571/62.	XX	PN
DE DR	XX	XX
PT PT	XX	PD 05-DEC-2002.
PT PT	XX	XX
PT PT	XX	PF 28-MAY-2002; 2002MO-US016789.
PT PT	XX	XX
PT PT	XX	PR 25-MAY-2001; 2001US-0293560P.
PT PT	XX	PR 21-JUN-2001; 2001US-0300187P.
PT PT	XX	PR 07-AUG-2001; 2001US-0310781P.
PT PT	XX	PR 17-SEP-2001; 2001US-0323662P.
PT PT	XX	PR 26-OCT-2001; 2001US-0344148P.
PT PT	XX	PR 15-NOV-2001; 2001US-0334674P.
PT PT	XX	PR 02-JAN-2002; 2002US-0346303P.
CC CC	XX	(DNAP-) DNAPRINT GENOMICS INC.
CC CC	XX	PA Example 17; Page 245; 36pp; English.
CC CC	XX	XX Prudakis T;
CC CC	XX	XX WPI; 2003-239091/23.
CC CC	XX	XX Inferring genetic pigmentation trait such as hair/eye color or shade from nucleic acid sample of human subject, by identifying a pigmentation-related haplotype allele of a pigmention gene in the sample.
CC CC	XX	XX PA Example 17; Page 245; 36pp; English.
CC CC	XX	XX The invention comprises a method for inferring a genetic pigmentation trait of a human. The method involves identifying a single nucleotide polymorphism (SNP) in a pigmention gene - where the pigmention gene is not melanocortin-1 receptor (MC1R) and agouti signalling protein (ASIP). The method of the invention is useful for inferring a genetic pigmentation trait of a human, especially for inferring the race of a human subject. The method is useful for inferring a genetic pigmentation trait such as hair shade or colour, or eye shade or colour of a human subject. The method may be used as a forensic tool for obtaining information relating to physical characteristics of a potential crime victim or a perpetrator of a crime from a nucleic acid sample present at a crime scene. The present PCR primer is used in the exemplification of the invention.
CC CC	XX	XX Sequence 45 BP; 13 A; 12 C; 15 G; 5 T; 0 U; 0 Other;
CC CC	XX	XX Query Match 3.0%; Score 20; DB 7; Length 45;
CC CC	XX	XX Best Local Similarity 72.2%; Pred. No. 2.5e+05;
CC CC	XX	XX Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
CC CC	XX	XX Gaps 0;
CC CC	XX	Qy 72 TCTTGGGGCCCAAGTCCTCAGAGTGCCAGCAATGCGATCGA 107
CC CC	XX	Db 44 TCTTGTGGGCTTGTCCTCCACAGTGGCATCGA 9
CC CC	XX	Search completed: February 29, 2004, 12:01:11
CC CC	XX	Job time : 308.726 sec
CC CC	XX	339 TCCAGGAACTCTCTCATCCCCAAGACCTTCCTGAGCAATGCTGG 374
CC CC	XX	2 TGAGGCCCTGATCCCTGAGCAATGCTGG 37
Qy SQ	Score 20; DB 6; Length 41;	
Best Local Similarity 72.2%; Conservative 0; Mismatches 10; Indels 0; Gaps 0;		

GenCore version 5.1.6
(c) 1993 - 2004 Compugen Inc.

OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 11:48:29 ; Search time 67.9494 Seconds

(without alignments) 5488.301 Million cell updates/sec

Title: US-09-904-568-1_COPY_132_803

Perfect score: 672

Sequence: 1 atgtctgtttggggctgc.....gtgagcgccaaactgcaggac 672

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 27747546 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0% summaries

Listing first 45 summaries

Database : Issued Patents NA:*

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1: /cgn2_6/podata/2/ina/5A_COMB.seq;*
2: /cgn2_6/podata/2/ina/5B_COMB.seq;*
3: /cgn2_6/podata/2/ina/6A_COMB.seq;*
4: /cgn2_6/podata/2/ina/6B_COMB.seq;*
5: /cgn2_6/podata/2/ina/PCITS_COMB.seq;*
6: /cgn2_6/podata/2/ina/backfiles..seq;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
c 1	21.2	3.2	47	4	US-09-671-317-808	Sequence 808, APP	SEQ ID NO: 808
c 2	20.6	3.1	47	4	US-09-671-317-639	Sequence 639, APP	LENGTH: 47
c 3	20.6	3.0	35	4	US-09-514-2474-2	Sequence 2, APP	TYPE: DNA
c 4	20	3.0	50	1	US-08-171-389-463	Sequence 463, APP	ORGANISM: Homo sapiens
c 5	20	3.0	50	2	US-08-123-936-463	Sequence 463, APP	FEATURE:
c 6	20	3.0	50	2	US-08-475-2284-463	Sequence 463, APP	NAME/KEY: allele
c 7	20	3.0	50	3	US-08-482-080-463	Sequence 463, APP	LOCATION: 24
c 8	20	3.0	50	4	US-09-354-947-463	Sequence 463, APP	OTHER INFORMATION: 12-132-437 : polymorphic base A or C
c 9	20	3.0	50	5	PCT-US3-12388-463	Sequence 463, APP	US-09-671-317-808
c 10	19.8	2.9	46	3	US-09-252-292-22	Sequence 463, APP	Query Match Score 3.2%; Best Local Similarity 65.9%; Matches 29, Conservative 1, Mismatches 14; Indels 0; Gaps 0;
c 11	19.2	2.9	44	4	US-08-617-785-19	Sequence 463, APP	RESULT 2
c 12	19.2	2.9	44	4	US-09-817-464-19	Sequence 463, APP	US-09-671-317-639
c 13	19.2	2.9	47	4	US-09-422-978-4676	Sequence 463, APP	Sequence 15, APP
c 14	19	2.8	27	2	US-08-859-998-80	Sequence 80, APP	Sequence 15, APP
c 15	19	2.8	27	4	US-09-225-928-80	Sequence 80, APP	Sequence 15, APP
c 16	19	2.8	27	4	US-09-25-2018-80	Sequence 15, APP	Sequence 17, APP
c 17	18.6	2.8	43	3	US-09-292-071-15	Sequence 6, APP	GENERAL INFORMATION:
c 18	18.6	2.8	43	3	US-08-732-708C-6	Sequence 7, APP	Applicant: Blumenfeld, Marta
c 19	18.6	2.8	43	3	US-09-292-069A-15	Sequence 15, APP	Applicant: Chumakov, Ilya
c 20	18.6	2.8	43	3	US-09-418-721-15	Sequence 15, APP	Applicant: Bougelieret, Lydie
c 21	18.6	2.8	43	4	US-09-767-013-15	Sequence 15, APP	Applicant: Bougelieret, Lydie
c 22	18.6	2.8	43	4	US-09-292-072-15	Sequence 15, APP	Applicant: Bougelieret, Lydie
c 23	18.4	2.7	31	1	US-09-556-601-17	Sequence 7, APP	Applicant: Bougelieret, Lydie
c 24	18.4	2.7	37	1	US-08-428-733A-7	Sequence 39, APP	Applicant: Bougelieret, Lydie
c 25	18.4	2.7	37	1	US-09-428-733A-39	Sequence 22, APP	Applicant: Bougelieret, Lydie
c 26	18.4	2.7	47	1	US-09-336-132-12	Sequence 48, APP	Applicant: Bougelieret, Lydie
c 27	18.2	2.7	40	1	US-09-195-874-4	Sequence 4, APP	Applicant: Bougelieret, Lydie

ALIGNMENTS

c 28	18.2	2.7	45	1	US-08-176-412-5	Sequence 5, APP
c 29	18.2	2.7	45	2	US-08-555-268A-5	Sequence 5, APP
c 30	18.2	2.7	45	2	US-08-495-695B-5	Sequence 5, APP
c 31	18.2	2.7	45	5	PCT-US94-14436-5	Sequence 5, APP
c 32	18.2	2.7	47	1	US-08-171-389-74	Sequence 74, APP
c 33	18.2	2.7	47	1	US-08-123-936-74	Sequence 74, APP
c 34	18.2	2.7	47	3	US-08-475-228A-74	Sequence 74, APP
c 35	18.2	2.7	47	3	US-08-482-080A-74	Sequence 74, APP
c 36	18.2	2.7	47	4	US-09-354-947-74	Sequence 74, APP
c 37	18.2	2.7	47	4	US-09-671-317-788	Sequence 74, APP
c 38	18.2	2.7	47	4	PCT-US93-12388-74	Sequence 74, APP
c 39	18	2.7	39	3	US-09-262-773-78	Sequence 839, APP
c 40	18	2.7	47	4	US-09-422-978-1159	Sequence 115%, APP
c 41	18	2.7	50	2	US-09-989-394-12	Sequence 12, APP
c 42	18	2.7	50	2	US-09-271-365-12	Sequence 12, APP
c 43	18	2.7	50	4	US-09-604-013A-12	Sequence 12, APP
c 44	18	2.6	40	1	US-09-195-874-4	Sequence 4, APP

RESULT 1

US-09-671-317-808/C	; Sequence 808, Application US/09671317
	; Patent No. 6528200
	; GENERAL INFORMATION:
	; APPLICANT: Blumenfeld, Marta
	; BOURGELIERET, Lydie
	; ATTORNEY: Cohen, Annick
	; TITLE OF INVENTION: BIALLERIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
	; FILE REFERENCE: 62.US3.CIP
	; CURRENT APPLICATION NUMBER: US/09/671-317
	; PRIORITY FILING DATE: 2000-09-27
	; PRIOR APPLICATION NUMBER: US/09/536,178
	; PRIOR FILING DATE: 2000-03-23
	; PRIOR FILING DATE: 2000-03-24
	; PRIOR FILING DATE: 1999-03-25
	; PRIOR APPLICATION NUMBER: US 60/126,269
	; PRIOR FILING DATE: 1999-04-30
	; NUMBER OF SEQ-ID NOS: 977
	; SOFTWARE: Patent.pm

US-09-671-317-808	Query Match Score 3.2%; Best Local Similarity 65.9%; Matches 29, Conservative 1, Mismatches 14; Indels 0; Gaps 0;
Qy	96 AGTGAAGCCGTGGCTCGTCAGCTTGAAGGACTTACAGAGGCA 139
Db	44 AGCGATGCCCTGGGCAGAKTTGGGGAGGGCAAGGAGCA 1
	RESULT 2

US-09-671-317-639	; Sequence 639, Application US/09671317
	; Patent No. 6528260
	; GENERAL INFORMATION:
	; APPLICANT: Blumenfeld, Marta
	; ATTORNEY: Cohen, Annick
	; TITLE OF INVENTION: BIALLERIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
	; FILE REFERENCE: 62.US3.CIP
	; CURRENT APPLICATION NUMBER: US/09/671-317
	; PRIORITY FILING DATE: 2000-09-27
	; PRIOR APPLICATION NUMBER: US/09/536,178
	; PRIOR FILING DATE: 2000-03-23
	; PRIOR FILING DATE: 2000-03-24
	; PRIOR FILING DATE: 1999-03-25
	; PRIOR APPLICATION NUMBER: US 60/131,961
	; PRIOR FILING DATE: 1999-04-30
	; NUMBER OF SEQ-ID NOS: 977
	; SOFTWARE: Patent.pm

APPLICANT: Cohen, Annick
 TITLE OF INVENTION: BIALLILEIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
 FILE REFERENCE: 62.US3.CIP

CURRENT APPLICATION NUMBER: US 09/671,317
 PRIOR APPLICATION NUMBER: US 09/536,178
 PRIOR APPLICATION NUMBER: PCT/IB00/00403
 PRIOR FILING DATE: 2000-03-27
 PRIOR FILING DATE: 2000-03-23
 PRIOR FILING DATE: 2000-03-24
 PRIOR FILING DATE: 1999-03-25
 PRIOR APPLICATION NUMBER: US 60/126,269
 PRIOR FILING DATE: 1999-04-30
 NUMBER OF SEQ ID NOS: 977
 SOFTWARE: Patent .pm
 SEQ ID NO: 639.
 LENGTH: 47
 TYPE: DNA
 ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: allele
 LOCATION: 24
 OTHER INFORMATION: 10-260-282 : polymorphic base G or T
 US-09-671-317-639

Query Match Score 20.6%; DB 4; Length 47;
 Best Local Similarity 64.4%; Pred. No. 3.5e+03;
 Matches 29; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

Qy	596 AGCTGGGTACAGTAGCCCTTGGCCTTAAGGGAGATGCCAGAAC 640
Db	3 AGGTAGGGACAGTGAGCATGGGGCCAGGAGCTGCCAGAGC 47

RESULT 3
 US-09-514-247A-2
 Sequence 2, Application US/09514247A
 Patent No. 6365361
 GENERAL INFORMATION
 APPLICANT: TANABE SEIYAKU CO. LTD.
 APPLICANT: TANIGUCHI, Junko
 TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPA
 FILE REFERENCE: TANIGUCHI=6
 CURRENT APPLICATION NUMBER: US/09/514,247A
 CURRENT FILING DATE: 2000-02-28
 PRIOR APPLICATION NUMBER: PCT/JP98/03734
 PRIOR FILING DATE: 1998-08-24
 PRIOR APPLICATION NUMBER: JP31084/1997
 PRIOR FILING DATE: 1999-08-27
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 2
 LENGTH: 35
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Artificially synthesized primer sequence

Query Match Score 20.2%; DB 4; Length 35;
 Best Local Similarity 75.8%; Pred. No. 4e+03;
 Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 86 CCTCTCCA GAAGTGACGGCGTGGCTCAGCTCT 118
 Db 1 CCGCTCAA GAATGTTGGCACTGGCTCAGGACT 33

RESULT 4
 US-08-171-389-463/C
 Sequence 463, Application US/08171389
 Patent No. 5578444
 GENERAL INFORMATION
 APPLICANT: Edwards, Cynthia A.
 APPLICANT: Cantor, Charles R.

GENERAL INFORMATION:
 APPLICANT: Edwards, Cynthia A.
 APPLICANT: Cantor, Charles R.
 APPLICANT: Andrews, Beth M.
 APPLICANT: Thirin, Lisa M.
 APPLICANT: Fly, Kirk E.
 TITLE OF INVENTION: Sequence-Directed DNA Binding Molecules, Compositions and Methods
 NUMBER OF SEQUENCES: 641.
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genelabs Technologies, Inc.
 STREET: 505 Penobscot Drive
 CITY: Redwood City
 STATE: CA
 COUNTRY: USA
 ZIP: 94063
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-OS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/171,389
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/123,936
 FILING DATE: 17-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/996,783
 FILING DATE: 23-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/723,618
 FILING DATE: 27-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/081,070
 FILING DATE: 22-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 463:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (Genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human insulin-like growth factor II
 INDIVIDUAL ISOLATE: gene
 US-08-171-389-463

Query Match Score 20%; DB 1; Length 50;
 Best Local Similarity 65.9%; Pred. No. 5.5e+03;
 Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 259 GCGGGCACACACACCCCTGCTCCAGAGGCTCTCCACCTGCC 302
 Db 49 GCGGGCCACGGCCAGCCGGCTATACTGCGCAACCCGCC 6

RESULT 5
 US-08-123-936-463/C
 Sequence 463, Application US/08123936
 Patent No. 5726014
 GENERAL INFORMATION:
 APPLICANT: Edwards, Cynthia A.
 APPLICANT: Cantor, Charles R.

APPLICANT: Andrews, Beth M.
 APPLICANT: Turin, Lisa M.
 TITLE OF INVENTION: Screening Assay for the Detection of
 NUMBER OF SEQUENCES: 640
 CORRESPONDENCE ADDRESS:
 ADDRESS: Genelabs Technologies, Inc.
 STREET: 505 Penobscot Drive
 CITY: Redwood City
 STATE: CA
 COUNTRY: USA
 ZIP: 94063

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/123,936
 FILING DATE: 27-JUN-1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/723,618
 FILING DATE: 27-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE DOCKET NUMBER: 4600-0075.32/G19P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 463:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human insulin-like growth factor II
 INDIVIDUAL ISOLATE: gene
 US-08-123-936-463

Query Match 3.0% Score 20; DB 1; Length 50;
 Best Local Similarity 65.9%; Prd. No. 5.5e+03; Indels 0;
 Matches 29; Conservative 0; Mismatches 15; Gaps 0;

Qy 259 GCGGGCACACACACCCCTGCTCCAGCAGGTCTCCGGTCTCCGG 302
 Db 49 GCGGAGCCACGCCACGCCGGCTTATAGTCGCGCAGCCGGCC 6

RESULT 6
 US-08-475-228A-463/C
 Sequence 463, Application US/08475228A
 Patent No. 5869241

GENERAL INFORMATION:
 APPLICANT: Edwards, Cynthia A.
 APPLICANT: Cantor, Charles R.
 APPLICANT: Andrews, Beth M.
 APPLICANT: Turin, Lisa M.
 APPLICANT: FLY, Kirk E.

TITLE OF INVENTION: Sequence-Directed DNA Binding
 Molecules, Compositions and Methods
 NUMBER OF SEQUENCES: 664

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genelabs Technologies, Inc.
 STREET: 505 Penobscot Drive
 CITY: Redwood City
 STATE: CA
 COUNTRY: USA
 ZIP: 94063

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,080A
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/171,389
 FILING DATE: 20-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/123,936
 FILING DATE: 17-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/723,618
 FILING DATE: 27-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/081,070
 FILING DATE: 22-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Brady, John F.
 REGISTRATION NUMBER: 39,118
 REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 324-0880
 TELEFAX: (650) 324-0960
 INFORMATION FOR SEQ ID NO: 463:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human insulin-like growth factor II
 INDIVIDUAL ISOLATE: gene
 US-08-482-080A-463

Query Match 3.0%; Score 20; DB 3; Length 50;
 Best Local Similarity 65.9%; Pred. No. 5.5e+03;
 Matches 29; Conservative 0; Mismatches 15; Indels 0;
 Gaps 0;

Qy	259	GCGGCAACACACCCCTGGCTCCAGCAGGTCTCCGGGCTGCCGCC	302
Db	49	GCGGCAACACGGCGCTTATAGTCGGCAAGCGCGCC	6

RESULT 8

Sequence 463, Application US/09354947
 Parent No. 6384208
 GENERAL INFORMATION:
 APPLICANT: Edwards, Cynthia A.
 APPLICANT: Cantor, Charles R.
 APPLICANT: Andrews, Beth M.
 APPLICANT: Turin, Lisa M.
 APPLICANT: Fry, Kirk E.
 TITLE OF INVENTION: Sequence-Directed DNA Binding
 NUMBER OF SEQUENCES: 664
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genelabs Technologies, Inc.
 STREET: 505 Penobscot Drive
 STATE: CA USA
 ZIP: 94063
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/354,947
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/482,080
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/171,389
 FILING DATE: 20-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/123,936
 FILING DATE: 17-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/723,618
 FILING DATE: 27-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/081,070
 FILING DATE: 22-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Brady, John F.
 REGISTRATION NUMBER: 39,118
 REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 324-0880
 TELEFAX: (650) 324-0960
 INFORMATION FOR SEQ ID NO: 463:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human insulin-like growth factor II
 US-09-354-947-463

Query' Match 3.0%; Score 20; DB 4; Length 50;
 Best Local Similarity 65.9%; Pred. No. 5.5e+03;
 Matches 29; Conservative 0; Mismatches 15; Indels 0;
 Gaps 0;

Qy	259	GCGGCAACACACCCCTGGCTCCAGCAGGTCTCCGGGCTGCCGCC	302
Db	49	GCGGCAACACGGCGCTTATAGTCGGCAAGCGCGCC	6

RESULT 9

PCT-US93-12388-463/c
 Sequence 463, Application PC/TUS9312388
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: Sequence-Directed DNA Binding
 NUMBER OF SEQUENCES: 641
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genelabs Technologies, Inc.
 STREET: 505 Penobscot Drive
 CITY: Redwood City
 STATE: CA
 COUNTRY: USA
 ZIP: 94063
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/12388
 FILING DATE: Sequence 19, Application US/08617785E
 CLASSIFICATION: Patent No. 6228610
 GENERAL INFORMATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/123,935
 FILING DATE: 17-SEP-1993
 ; APPLICANT: Flor, Peter J.
 ; APPLICANT: Kuhn, Ranier
 ; APPLICANT: Lindaur, Kristen
 ; APPLICANT: Puttnar, Irene
 ; APPLICANT: Knopfel, Thomas
 TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33, 875
 REFERENCE/DOCKET NUMBER: 4600-0175.41/G19FCT2
 TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 ; APPLICANT: Knopfel, Thomas
 ; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR7) and Related DNA Compounds
 ; FILE REFERENCE: 4-19679/A/PCT
 CURRENT APPLICATION NUMBER: US/08/617,785E
 CURRENT FILING DATE: 1996-03-19
 ; CURRENT APPLICATION NUMBER: PCT/EP94/02991
 ; EARLIER APPLICATION NUMBER: PCT/EP94/02991
 ; EARLIER FILING DATE: 1994-09-07
 ; EARLIER APPLICATION NUMBER: EPO 9416553.7
 ; EARLIER FILING DATE: 1994-08-19
 ; EARLIER APPLICATION NUMBER: EPO 93810663.0
 ; EARLIER FILING DATE: 1993-09-20
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 19
 ; LENGTH: 44
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: Oligonucleotide Primer
 US-08-617-785-19

RESULT 10
 US-09-252-292-22
 Query Match Score 20; DB 5; Length 50;
 Best Local Similarity 65.9%; Pred. No. 5.5e+03;
 Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 Qy 259 GCGGGCAACACACCCGCTTCCAGAGGTCTCGGCTGCC 302
 Db 49 GCGGGCACCACGGCCGGCTTATAGTCGGCCAGCCGGCC 6

Query Match Score 20; DB 5; Length 50;
 Best Local Similarity 65.9%; Pred. No. 5.5e+03;
 Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 Qy 259 GCGGGCAACACACCCGCTTCCAGAGGTCTCGGCTGCC 302
 Db 49 GCGGGCACCACGGCCGGCTTATAGTCGGCCAGCCGGCC 6

RESULT 11
 US-09-252-292-22
 Query Match Score 19.8%; DB 3; Length 46;
 Best Local Similarity 69.2%; Pred. No. 6.1e+03;
 Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Qy 550 GATGGACTGACACGGCTTGAGGTGCCTAGCCAA 588
 Db 4 GATGGACTGACACGGCTTGAGGTGCCTAGCCAA 42

Query Match Score 19.8%; DB 3; Length 46;
 Best Local Similarity 69.2%; Pred. No. 6.1e+03;
 Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Qy 550 GATGGACTGACACGGCTTGAGGTGCCTAGCCAA 588
 Db 4 GATGGACTGACACGGCTTGAGGTGCCTAGCCAA 42

RESULT 12
 US-09-817-464-19/C
 Query Match Score 19.2%; DB 3; Length 44;
 Best Local Similarity 67.5%; Pred. No. 9.2e+03;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 Qy 266 CACACACCTGCTCCAGAGGTCTCGGCTGCCCTGTC 305
 Db 42 CCCGCTCTAGCCCTAGGCCCCCTGGCCCTGGCCCTGAGC 3

Query Match Score 19.2%; DB 3; Length 44;
 Best Local Similarity 67.5%; Pred. No. 9.2e+03;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 Qy 266 CACACACCTGCTCCAGAGGTCTCGGCTGCCCTGTC 305
 Db 42 CCCGCTCTAGCCCTAGGCCCCCTGGCCCTGGCCCTGAGC 3

RESULT 13
 US-09-817-464-19/C
 Query Match Score 19.2%; DB 3; Length 44;
 Best Local Similarity 67.5%; Pred. No. 9.2e+03;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 Qy 266 CACACACCTGCTCCAGAGGTCTCGGCTGCCCTGTC 305
 Db 42 CCCGCTCTAGCCCTAGGCCCCCTGGCCCTGGCCCTGAGC 3

Query Match Score 19.2%; DB 4; Length 44;
 Best Local Similarity 67.5%; Pred. No. 9.2e+03;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 Qy 266 CACACACCTGCTCCAGAGGTCTCGGCTGCCCTGTC 305
 Db 42 CCCGCTCTAGCCCTAGGCCCCCTGGCCCTGGCCCTGAGC 3

RESULT 14
 US-09-817-464-19/C
 Query Match Score 19.2%; DB 4; Length 44;
 Best Local Similarity 67.5%; Pred. No. 9.2e+03;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 Qy 266 CACACACCTGCTCCAGAGGTCTCGGCTGCCCTGTC 305
 Db 42 CCCGCTCTAGCCCTAGGCCCCCTGGCCCTGGCCCTGAGC 3

Query Match Score 19.2%; DB 4; Length 44;
 Best Local Similarity 67.5%; Pred. No. 9.2e+03;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 Qy 266 CACACACCTGCTCCAGAGGTCTCGGCTGCCCTGTC 305
 Db 42 CCCGCTCTAGCCCTAGGCCCCCTGGCCCTGGCCCTGAGC 3

RESULT 13
US-09-422-978-2676

Sequence 266 CACACCCCTGGCTCCAGGAGGCTCTCCGGCTGCCCTTGC 305
Patent No. 6537751

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

CURRENT APPLICATION NUMBER: US/09/422,978
EARLIER APPLICATION NUMBER: US 99-10-20
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 2676
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
OTHER INFORMATION: 99-13864-64 : polymorphic base G or T

US-09-422-978-2676

Query Match 2.9% Score 19.2; DB 4; Length 47;
Best Local Similarity 70.6%; Pred. No. 9.5e+03;
Matches 24; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 272 CCTCTGCTTAGCGGGCTCTCCGGCTGCCCTG 305
Db 10 CCCCTCCACAGCTGCTCCCTCCCTTG 43

RESULT 14
US-08-859-998-80/C

Sequence 80, Application US/08859998
Patent No. 594076

GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
STATE: CA
COUNTRY: US
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.

REGISTRATION NUMBER: 37 620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5970
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
; SEQ ID NO: 80;
; US-09-225-928-80

Query Match 2 8%; Score 19; DB 4; Length 27;
Best Local Similarity 81.5%; Pred. No. 8.3e+03;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 43 GCTGACAGTCAACAGCGCCGGTCACT 69
||| ||||| ||||| |||||
Db 27 GCAGACAGTCACACTGGTTGGTCACT 1

Search completed: February 29, 2004, 14:42:39
Job time : 70.9494 sec

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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 09:53:57 ; Search time 303.274 Seconds

Title: US-09-904-568-1_COPY_132_803

Prefect score: 672 Sequence: 1 atgtcgcttggggctgc.....gttagcgaaactgcaggac 672

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2001s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003as:*

10: Geneseqn2004s:*

ALIGNMENTS

RESULT 1 ABA99919.C

ID ABA99919 standard; DNA; 49 BP.

XX ABA99919;

AC XX

DT 05-JUL-2002 (first entry)

XX Human TNF PCR primer SEQ ID 13.

XX DE

XX XX

Produug; TNF; tumour necrosis factor; selectokine; chimerica; W24; W33; cytostatic; immunomodulatory; antiangiogenic; apoptosis inducer; gene therapy; scFv antibody OS4; fibroblast activation protein; tenascin; solid tumour; angiogenesis; treatment; infection; metabolic disease; PCR; primer; ss.

XX Homo sapiens.

XX WO200222833-A1.

XX PN

XX XX

XX 21-MAR-2002.

XX PD

XX PP

XX 17-SEP-2001; 2001WO-EP010730.

XX PR

XX 15-SEP-2000; 2000DE-01045592.

XX PA

XX (UYST-) UNIV STUTTGART.

XX PA (PFZ12) PFIZENMAIER K.

XX XX

XX PI

XX Pfizenmaier K,

XX Wuest T,

XX Moosmayer D,

XX Grell M,

XX Scheurich P;

XX DR

XX WPI; 2002-362351/39.

XX PT

XX New polypeptide prodrug, useful e.g. for treating tumors, contains

XX targeting region, active agent and attached inhibitor that is

XX proteolytically cleaved in target cells.

XX Example 6; Page 47; 52PP; German.

XX This invention describes a novel polypeptide (I) comprising, in the N to

CC C direction, a region (R1) that recognises selectively a specific

CC macromolecule on a cell surface and/or a component of the extracellular

CC matrix, peptide linker, a region (R2) with biological activity for a

CC specific target molecule, a region (R3) that has a processing site and a

CC region (R4) that inhibits the activity of R2, by intramolecular bonding

CC and/or interaction. The products of the invention have cytostatic,

CC

</

immunomodulatory and antiangiogenic activity, induce apoptosis and can be used for gene therapy. My-1 cells (20000) were incubated with the prodrug W24, containing, essentially, the single-chain Fv antibody OS4, specific for human fibroblast activation protein, trimerization linker, mutant form of the tumour necrosis factor (TNF) precursor protein, a region with a proteolytic cleavage site, and human TNF receptor-1 fragment and with trypsin (activator) for 5 minutes. After 16 hours, cell viability was determined by MTT staining. Activated W24 had LD50 about 0.5 ng/ml, comparable with that for wild-type TNF and 400 times higher than for uncleaved W24. (II), also nucleic acids encoding them and related vectors, are useful particularly for treating solid tumours and/or pathological angiogenesis, also generally for treating infections and metabolic diseases. (II) are prodrug forms of R2 that have unacceptable toxicity when administered systemically (specifically tumour necrosis factor) and allow these compounds to be administered safely with retention of, or even increase in, therapeutic activity. R2 is released only in target tissue, resulting in a high local concentration, and activity is potentiated by co-activation of receptors. This sequence represents a PCR primer for the amplification of the human TNF fragment used in the construction of the TNF-selcetokine W24 and W33 prodrugs described in the disclosure of the invention.

	Sequence 49 BP; 12 A; 15 C; 12 G; 10 T; 0 U; 0 Other;	Query Match	Score 21.8;	DB 6;	Length 49;
Q		Best Local Similarity	3.2%;	Pred. No.	2.6e+04;
		Matches	70.7%;	Mismatches	2.6e+04;
		29;	Conservative	0;	Indels
				12;	Gaps 0
Y	TGGGTATCCAGGCTTCAGAAGTACGGCGTGAGTCAG 114	74	TGGGTATCCAGGCTTCAGAAGTACGGCGTGAGTCAG 114		
b	TGGGATCATTCATGCCCTGCGGATCAGGGTGTGATCCG 6	46	TGGGATCATTCATGCCCTGCGGATCAGGGTGTGATCCG 6		

RESULT 2	BZ24835			
D	ABZ24835 standard; DNA; 50 BP.			
X				
C	ABZ24835;			
X				
X		03-MAR-2003 (first entry)		
T				
X				
X				
X				
W				
W				
W				
W				
W				
W				
X				
S				

N N JP2002247986-A.
X X
D D 03-SBP-2002.
X X
F F 23-FBB-2001; 20001JP-00048876.
X X
R R 23-FBB-2001; 20001JP-00048876.

VA (MITA) MITSUI CHEM INC.
X X WPI; 2003-096457/09.
X X Cells for evaluation of agonistic and antagonistic activ-
X X nuclear receptor of a substance, comprise a stable expe-
X X rt of an intranuclear receptor gene and a reporter gene.
X X Example 4; Page 11; 33PP; Japanese.

The present invention relates to cells obtained by introduction of a reporter expression nucleic acid, which comprises a response element and a promoter downstream of the response element. The promoter controls transcription in animal host cells to significantly stimulate the expression of the reporter gene in the presence of a ligand bound to an intranuclear receptor. The cells are used for evaluation of a sex hormone receptor e.g. androgen receptor (AR) and oestrogen receptor (ER), and

	Query	Match	Score	Length	DB	Indels	Gaps
CC	Sequence 50 BP; 7 A; 12 C; 18 G; 13 T; 0 U; 0 Other;	Best Local Similarity	3.2%	Score 21.4;	DB 7;	Length 50;	
CC	Matches 31; Conservative 0; Mismatches 16; Gaps 0;	Matches 31;	Conservative 0;	Mismatches 16;	Gaps 0;		
CC		Pred. No. 3.4+04;					
CC		Indels 0;					
XX							
SQ							
Qy	136 AGCAGCTTCGAAATTGTGAAGACTGAGTGGGCCCTGCATCG	182					
Db	4 AGCTCTGGCCACCCGTGACGTGTAAAGCGGTGCTGTGAGG	50					

XX	PN	WO200043528-A1.
XX	PD	27-JUL-2000.
XX	PF	25-JAN-2000;
XX	PR	25-JAN-1999;
XX	PA	99JUP-00015667.

(KUROKA /) KUROKAWA K.
 (KUROKA /) KUROKAWA M.
 (KUROKA /) KUROKAWA T.

XX	Miyata T;
PT	
XX	
DR	WPI; 2000-543257/49.
XX	
PT	DNA for promoter region of megsin useful for screening proteins.
XX	
DS	Example 5. Page 38. 45mm: Japanese.

This invention describes a novel DNA sequence (I) representing a promoter region having part or all of a specific base sequence. The invention also describes (1) a vector containing (I); (2) a cell transformed by the above vector; and (3) protein produced using (I). (I) is useful for screening and isolating proteins (especially transcription factors) ABA7134-A71469 represent PCR primers used in the method described in the invention.

RESULT 4
ABL40388/C
ID ABL40388 Standard; cDNA; 33 BP.
XX ABL40388;
AC
VV

DT 01-JUL-2002 (first entry)
 XX Primer 3 relative to HOMO phosphoryl transport protein 12.
 DE KW HOMO phosphoryl transport protein 12; cancer; haemopathy; phlogosis;
 KW immune disease; HIV; human immunodeficiency virus; cytotoxic;
 KW haemostatic; virucide; immunomodulatory; antiinflammatory;
 KW gene therapy; malignant tumour; PCR; primer; ss.
 XX Unidentified.
 XX WO200200698-A1.
 XX 03-JAN-2002.
 PD 14-MAY-2001; 2001WO-CN000793.
 XX 16-MAY-2000; 2000CN-00115689.
 XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 PA PI Mao Y, Xie Y;
 XX DR 2002-075663-10.
 XX PT Polypeptide-HOMO phosphoryl transport protein 12 and encoding
 PT polynucleotide, used in diagnosis and treatment of malignant tumors,
 PT hemopathy, human immunodeficiency virus infection, immunological diseases
 PT and inflammation.
 PS Example 4; Page 18; 37BP; Chinese.
 XX The invention relates to an isolated polypeptide of polypeptide-HOMO
 CC phosphoryl transport protein 12. The activity of the polypeptide of the
 CC invention may be described as, cytosstatic, haemostatic, virucide,
 CC immunomodulatory and antiinflammatory. Polypeptides and polynucleotides
 CC of the invention are used in diagnosis and treatment of malignant tumour,
 CC haemopathy, human immunodeficiency virus (HIV) infection, immunological
 CC diseases various inflammations, and phlogosis. They may also be used in
 CC gene therapy. The current sequence represents a primer relative to the
 HOMO phosphoryl transport Protein 12 of the invention.
 XX Sequence 33 BP; 5 A; 9 C; 13 G; 6 T; 0 U; 0 Other;
 SQ Score 21; DB 6; Length 33;
 Query Match 3.1%; Pred. No. 3.8e+04;
 Best Local Similarity 82.8%;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 280 CAGCAGGCTCTCCGGTGGCCCTGCTAG 308
 Db 33 CACCGGGCTCAGGGCCCATGCTAG 5
 PS Example 1; Page 9; 12pp; Japanese.

XX PR 19-MAR-1996; 96JP-00062885.
 XX PA (SUMIQ) SUMITOMO METAL IND LTD.
 XX DR WPI; 1997-540228/50.
 PT Solid phase gene - useful for detection of genes in a sample.
 XX PS Example 1; Page 9; 12pp; Japanese.

XX The present sequence represents a DNA probe which is used to demonstrate
 CC a new method for the detection of genes, using a synthetic gene in the
 CC solid phase. The gene has a (substituted) trityl group which binds to a
 CC hydrophobic carrier through an end protective group. The method is simple
 CC and the solid phased gene is stable. Gene amplification was carried out
 CC using a primer set to contain a point mutation determining each ant-gen
 CC type in the amplification region for HPA-1 to HPA-6. A synthetic DNA was
 CC prepared and a probe was immobilised on the plate. The present probe
 CC binds to HPA-2
 XX SQ Sequence 40 BP; 7 A; 9 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 3.1%; Score 21; DB 2; Length 40;
 Best Local Similarity 73.0%; Pred. No. 4.1e+04;
 Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 308 GTCTAAAGCCAGATGCCCTCCAGGAAGGTCCACCA 344
 Db 4 GCCTTAGCTCATGCCTTCAGTTAGCTCTTGAA 40

RESULT 6
 AAQ52858
 ID AAQ52858 standard; RNA; 42 BP.
 XX
 AC AAQ52858;
 XX DT 25-MAR-2003 (revised)
 DT 26-MAY-1994 (First entry)

Cytomegalovirus target sequence 35.
 DE XX RNA; enzyme; enzymatic RNA molecule; cleave; RNA; mRNA; HnRNA;
 KW picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
 KW Papilloma virus; HPV; Epstein-Barr virus; EBV; TCLV;
 KW T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
 KW influenza virus; HSV; herpes simplex virus; vector; immune response;
 KW antibody; ribozyme; viral RNA; treatment; ss.
 XX OS Synthetic.
 XX PN WO9323569-A1.
 XX PD 25-NOV-1993.
 XX PF 29-APR-1993; 93WO-US004020.

RESULT 5
 AAT89030
 ID AAT89030 standard; DNA; 40 BP.
 AC AAT89030;
 XX DT 04-FEB-1998 (first entry)
 XX DE Solid phase gene HPA-2 DNA probe.
 XX KW Solid phase gene; synthetic gene; gene synthesis; trityl group;
 KW hydrophobic carrier; PCR primer; detection probe; HPA; ss.
 XX OS Synthetic.
 XX PN JP09257798-A.
 PD 03-OCT-1997.
 XX PR 19-MAR-1996; 96JP-00062885.
 PP 19-MAR-1996; 96JP-00062885.
 PR 14-MAY-1992; 92US-00882886.
 PR 14-MAY-1992; 92US-00882887.
 PR 14-MAY-1992; 92US-00882713.
 PR 14-MAY-1992; 92US-00882714.
 PR 14-MAY-1992; 92US-00882823.
 PR 14-MAY-1992; 92US-00882824.
 PR 14-MAY-1992; 92US-00882886.
 PR 14-MAY-1992; 92US-00882887.
 PR 14-MAY-1992; 92US-00882921.
 PR 14-MAY-1992; 92US-00882922.
 PR 14-MAY-1992; 92US-00883823.
 PR 14-MAY-1992; 92US-00883849.
 PR 14-MAY-1992; 92US-00884073.
 PR 14-MAY-1992; 92US-00884074.

PR 14-MAY-1992; 92US-00884333.
 PR 14-MAY-1992; 92US-00884412.
 PR 14-MAY-1992; 92US-00884416.
 PR 14-MAY-1992; 92US-00884521.
 PR 31-JUL-1992; 92US-00932718.
 PR 26-AUG-1992; 92US-00935854.
 PR 26-AUG-1992; 92US-00935856.
 PR 18-SEP-1992; 92US-00948359.
 PR 07-OCT-1992; 92US-00963322.
 PR 07-DEC-1992; 92US-00987129.
 PR 07-DEC-1992; 92US-00987130.
 PR 07-DEC-1992; 92US-00987133.
 XX (RIBO-) RIBOZYME PHARM INC.
 P1 Draper KG, Dudycz LW, Mcewigen JA, Maceják DG, Holecek JJ;
 P1 Mamone JA;
 XX DR; 1993-386599/48.
 XX Enzymatic RNA molecules - used to inhibit viral replication, infection
 PT and gene expression.
 XX P5; Fig 13; 287pp; English.
 XX The sequences (AQS2824-Q52890) are pref. Cytomegalovirus target
 CC sequences for enzymatic RNA molecules. The RNA molecules are
 complementary to a substrate binding region in the specified gene target.
 CC They also have enzymatic properties, in that they specifically cleave RNA
 CC in the target. The RNAs interfere with viral replication and therefore
 CC have anti-viral properties. They can be used to attenuate viruses to be
 CC used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct R field.) (Updated on 25-MAR-2003 to correct
 CC PI field.)
 XX Sequence 42 BP; 9 A; 9 C; 17 G; 0 T; 7 U; 0 Other;
 XX Query Match 3.1%; Score 20.8; DB 2; Length 42;
 Best Local Similarity 60.0%; Prd. No. 4.8e+04;
 Matches 24; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
 XX Qy 201 TGTTGAGGAACCTGGTGCAGGCCAACCTGTCAAGAGAG 240
 DB :||:||:||:||:||:||:||:||:||:||:||:||:||:
 2 UGGGAUCACTGGCCAUUGCCGAGUCAGAUGAG 41
 XX (TANABE) TANABE SEIYAKU CO.
 XX Rattus ratus.
 OS WO9704104-A2.
 XX 06-FEB-1997.
 XX 12-JUL-1996; 96WO-US011673.
 XX 14-JUL-1995; 95US-0001195P.
 XX (UYJO) UNIV. JOHNS HOPKINS
 XX Pedersen PL, Mathupala SP, Rempel A;
 PT

XX DR WPI; 1997-132643/12.
 XX PT New transcription regulating fragments of hexokinase II DNA contg.
 PT Response element - and methods for diagnosis or treatment of neoplasias
 PT that over-express hexokinase II and for regulating glycolysis.
 XX PS Claim 1; Fig 11; 104PP; English.
 XX The present sequence represents a segment of the hepatoma AS-30D Type II
 CC hexokinase promoter region. Response elements (transcription factor
 CC binding site) in this fragment may consist of all or part of the present
 CC sequence. AS-30D is a new isolated hexokinase II. The present DNA
 CC fragment is capable of regulating transcription of a downstream open
 CC reading frame and contains at least one response element. The present DNA
 CC fragment may be coupled to a reporter gene and used to screen for
 CC potential drugs that affect regulated transcription of tumour hexokinase
 CC II. Alternatively it may be coupled to a toxic gene and used to treat
 CC cells that over-express hexokinase II, such as those present in patients
 CC with cancer. It may also be used in gene therapy to treat diabetes. The
 CC DNA fragment increases glycolysis in cells and express homologous or
 CC heterologous protein. Probes of the DNA fragment are used in the method
 CC for diagnosing a neoplasia that over-expresses hexokinase. The new
 CC response elements are active only in tumours, not in normal cells.
 XX SQ Sequence 49 BP; 11 A; 21 C; 12 G; 5 T; 0 U; 0 Other;
 XX Query Match 3.1%; Score 20.8; DB 2; Length 49;
 Best Local Similarity 64.6%; Prd. No. 5e+04;
 Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 XX Qy 255 GCTGGGGCACACAACCCCTGCTCAGGGTCTGGCGTCGCC 302
 DB 2 GCGCGAGCGTACAACCCCTCTCCCCAGGCAATGAGCGCCAC 49
 XX PS RESULT 8
 AAX27583
 ID AAX27583 standard; DNA; 35 BP.
 XX ID AAX27583;
 AC AC
 XX DT 27-MAY-1999 (First entry)
 XX DT 27-AUG-1997; 97JP-0023104.
 XX DE PPAR cDNA amplifying primer 2.
 XX KW Peroxisome proliferator-activated receptor; PPAR; reporter Gene; CAT;
 KW transcriptional coupling factor; screening; CBF; SRC-1; lacZ;
 KW antidiabetic; obesity; PCR primer; ss.
 OS Synthetic.
 XX PN WO910534-A1.
 XX ID 04-MAR-1999.
 AC AC
 XX PD 04-MAR-1999.
 XX PF 24-AUG-1998; 98WO-JP003734.
 XX PR 27-AUG-1997; 97JP-0023104.
 XX PA (TANABE) TANABE SEIYAKU CO.
 XX PI Taniuchi T, Mizukami J;
 XX DR WPI; 1999-190635/16.
 XX PT Screening agonist/antagonists to peroxisome proliferator-activated
 PT receptor - by contacting with a test cell containing a suitable reporter
 PT gene.
 XX PS Example; Page 24; 34PP; Japanese.
 XX The invention relates to methods for identifying potential agonists or

XX XX (GENE-) GENELABS TECHNOLOGIES INC.
 PD PA XX PI Edwards CA, Cantor CR, Andrews BM, Turin LM, FRY KB;
 PF XX DR WPI; 1994-234711/28.
 XX PR Sequence-directed DNA-binding molecules - useful in pharmaceuticals and
 PT XX PR molecular reagents.
 XX PS XX Claim 28; Page 443; 58pp; English.
 DR XX A DNA protein-binding assay is provided, useful for screening libraries
 PT of synthetic or biological cpos, for their ability to bind DNA test
 PT sequences. The assay is versatile in that any number of test sequences
 PT can be tested by placing the test sequence adjacent to a defined protein-
 PT binding sequence. Binding of mols. to these test sequences
 PT changes the binding characteristics of the protein moi. to its cognate
 PT binding sequence. When such a mol. binds the test sequence, the
 PT equilibrium of the DNA:protein complexes is disturbed, generating changes
 PT in the concentration of free DNA probe. One application of this method is
 PT to eucaryotic general transcription factors (e.g. TFIID), where the
 PT target region is typically selected from DNA sequences adjacent to the
 PT binding site for the eucaryotic transcription factor. Numerous exemplary
 PT test sequences are given: the sequences in AAQ69251-731 and AAQ69850
 PT correspond to promoter targets (typically, TATA box-contg. sites) for
 PT human genes and the sequences in AAQ6932-859 correspond to promoter
 PT targets for viral genes. The test sequences may also be randomly
 PT generated. DNA:protein interaction may be used for screening purposes,
 PT e.g., the Herpes Simplex Virus (HSV) origin of replication and UL9 (see
 PT CC AAQ69851-52, AAQ69865 and AAQ69891). (Updated on 25-MAR-2003 to correct
 PT CC PN field.)
 XX SQ Sequence 50 BP; 6 A; 18 C; 21 G; 5 T; 0 U; 0 Other;
 CC AC Query Match 3.0%; Score 20; DB 2; Length 50;
 CC AC Best Local Similarity 65.9%; Pred. No. 8.6e+14;
 CC AC Matches 29; Conservative 0; Mismatches 15; Indels 0;
 CC AC Caps 0;
 CC QY 259 GCGGGCACACACCTGCTCCAGAGGCTTCGGCTGCC 302
 CC Db 49 GCGGGCCAGGCCAGCCGGCTCTATGTCGCCAGCCGGCC 6
 CC XX RESULT 13
 CC ID AAT64175/C
 CC ID AAT64175 standard; DNA; 50 BP.
 CC AC AC
 CC DT XX 25-MAR-2003 (revised)
 CC DT XX 17-MAR-1997 (first entry)
 CC DE XX Human insulin-like growth factor-II Gene TFIID binding site.
 CC KW XX Duplex DNA; target region; binding characteristic; DNA binding protein;
 CC KW TFIID; transcription factor; binding site; inhibition; enhance; cancer;
 CC DE XX inherited genetic disorder; ds.
 CC OS XX Homo sapiens.
 CC PN XX US5578444-A.
 CC XX PD 26-NOV-1996.
 CC XX PF 20-DEC-1993; 93US-00171189.
 CC XX PR 27-JUN-1991; 91US-00723618.
 CC XX PR 23-DEC-1992; 92US-00956983.
 CC PR 17-SEP-1993; 93US-00123936.
 CC PA XX (GENE-) GENELABS TECHNOLOGIES INC.
 CC PR XX

XX XX WO941980-A1.
 XX PD 07-JUL-1994.
 XX PR 20-DEC-1993; 93WO-US012338.
 XX PR 23-DEC-1992; 92US-00996793.
 XX PR 17-SEP-1993; 93US-00123936.

R WPI: 2002-442819/47

R WPI; 2002-442819/47.
X

Decreasing transcriptional activity of genes for treating infections or cancer, by administration of an agent that binds to two non-overlapping regions of the gene.

Example 15: SEO TD NO A63 : 982n: English

The invention relates to a method of decreasing transcriptional activity in a duplex deoxyribonucleic acid (DNA) template ($\text{t}1$) comprising contacting ($\text{T}1$) with a binding agent comprising at least one small duplex-DNA-binding molecule ($\text{T}2$) coupled to at least one other small duplex-binding molecule that binds to a non-overlapping region of target sequence ($\text{T}3$). The method is useful for inhibiting transcription of a range of disease-related genes for treating infections (by viruses, including human immunodeficiency virus, bacteria, fungi, protozoa and parasites), cancer, cardiovascular, respiratory, gastrointestinal, endocrine/metabolic, rheumatic/immunological, haematological, neurological, psychiatric, dermatological, ophthalmological, musculoskeletal, genetic or urogenital disorders. The method provides sequence-specific inhibition of transcription of pathological genes without affecting transcription of cellular genes regulated by the same transcription factor, and can be applied to regulation of any gene. AB82492-AB83155 represent DNA binding molecule test sequences used in the method of the invention.

SAMARITAN 50 RD.

Query Match 3.0%; Score 20; DB 6; Length 50;
 Best Local Similarity 65.9%; Prod. No. 8..6e+04;
 Matches 29; Conservative 0; Mismatches 15; Indels

25.9 GCGGCAACACACCCCTGCCTCCAGGGCTCCGGCTGCC 30

4.9 GGGGGGGGCAAGCCCCCTTATAGTCGGCCAGGCC 6

Search completed: February 29, 2004, 12:01:06

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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 11:52:38 ; Search time 268.199 Seconds
(without alignments)

Title: US-09-904-568-3_COPY_294_966

Perfect score: 673

Sequence: 1 aatgtctgtggggctg.....stgaggcgactgaggac 673

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 2353733 seqs, 1803733377 residues

Total number of hits satisfying chosen parameters: 1385142

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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1: /cgn2_6/ptodata/2/pubpna/us07_PUBCOMB.seq/*
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3: /cgn2_6/ptodata/2/pubpna/us06_NEW_PUB.seq/*
4: /cgn2_6/ptodata/2/pubpna/us06_PUBCOMB.seq/*
5: /cgn2_6/ptodata/2/pubpna/us07_NEV_PUB.seq/*
6: /cgn2_6/ptodata/2/pubpna/us08_PUBCOMB.seq/*
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8: /cgn2_6/ptodata/2/pubpna/us08_PUBCOMB.seq/*
9: /cgn2_6/ptodata/2/pubpna/us09A_PUBCOMB.seq/*
10: /cgn2_6/ptodata/2/pubpna/us09E_PUBCOMB.seq/*
11: /cgn2_6/ptodata/2/pubpna/us09C_PUBCOMB.seq/*
12: /cgn2_6/ptodata/2/pubpna/us09_NEW_PUB.seq/*
13: /cgn2_6/ptodata/2/pubpna/us10A_PUBCOMB.seq/*
14: /cgn2_6/ptodata/2/pubpna/us10B_PUBCOMB.seq/*
15: /cgn2_6/ptodata/2/pubpna/us10C_PUBCOMB.seq/*
16: /cgn2_6/ptodata/2/pubpna/us10_NEW_PUB.seq/*
17: /cgn2_6/ptodata/2/pubpna/us560_NEW_PUB.seq/*
18: /cgn2_6/ptodata/2/pubpna/us860_PUBCOMB.seq/*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
c 1	23	3.4	48	14 US-10-361-420-17	Sequence 37, Appl
c 2	20	3.0	50	9 US-09-736-969A-67	Sequence 67, Appl
c 3	20	3.0	50	15 US-10-131-827-3541	Sequence 3541, Ap
c 4	19.6	2.9	45	10 US-09-974-026-61	Sequence 61, Appl
c 5	19.6	2.9	48	10 US-09-780-533A-5931	Sequence 5931, Ap
c 6	19.6	2.9	50	15 US-10-131-827-4141	Sequence 4141, Ap
c 7	19.4	2.9	48	9 US-09-753-35-67	Sequence 67, Appl
c 8	19.4	2.9	48	14 US-10-156-306-7723	Sequence 7723, Ap
c 9	19.4	2.9	48	14 US-10-163-942-67	Sequence 67, Appl
c 10	19.4	2.9	50	9 US-09-874-547-6	Sequence 6, Appl
c 11	19.2	2.9	46	14 US-10-219-195-45	Sequence 45, Appl
c 12	19.2	2.9	50	15 US-10-131-827-6386	Sequence 6386, Ap
c 13	19.2	2.9	50	15 US-10-131-827-6776	Sequence 6776, Ap
c 14	19.2	2.9	36	9 US-09-140-668A-57	Sequence 57, Appl
c 15	19	2.8	38	12 US-10-429-849-12	Sequence 12, Appl

RESULT 1
US-10-361-420-37/C
; Sequence 37, Application US/10361420
; Publication No. US20030170866A1
; GENERAL INFORMATION:
; APPLICANT: Ruderman, Joan V.
; Herskoff, Avram
; Kirschner, Marc W.
; Townsley, Fiona
; Aristarkov, Alexander
; Bytan, Esther
; YU, Hongtao

TITLE OF INVENTION: NOVEL CYCLIN-SELECTIVE UBIQUITIN CARRIER
SEQUENCES: 37
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentNet Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/361,420
FILING DATE: 10-Feb-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/772,156
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/828,533
FILING DATE: 1997-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Kerner Ph.D., Ann-Louise

REGISTRATION NUMBER: 33,523
 REFERENCE/DOCKET NUMBER: HA2-015CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 526-6000
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 48 base Pairs
 TYPE: Nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: other nucleic acid
 FRAGMENT TYPE: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 37:
 US-10-361-420-37

RESULT 2
 US-09-736-969A-67/c
 Sequence 67, Application US/09736969A
 Patent No. US20030068302A1
 GENERAL INFORMATION:
 APPLICANT: Lu, Peter
 ATTORNEY OR AGENT: Garman, Jonathan David
 ATTORNEY OR AGENT: Candia III, Albert Frederick
 ATTORNEY OR AGENT: Arbor Vita Corporation
 TITLE OF INVENTION: CLASP-4 Transmembrane Protein
 FILE REFERENCE: 020054-000411US
 CURRENT FILING DATE: 2000-12-13
 PRIOR APPLICATION NUMBER: US 60/160,860
 PRIOR FILING DATE: 1999-10-21
 PRIOR APPLICATION NUMBER: US 60/162,498
 PRIOR FILING DATE: 1999-10-29
 PRIOR APPLICATION NUMBER: US 60/170,453
 PRIOR FILING DATE: 1999-12-13
 PRIOR APPLICATION NUMBER: US 60/176,195
 PRIOR FILING DATE: 2000-01-14
 PRIOR APPLICATION NUMBER: US 60/182,296
 PRIOR APPLICATION NUMBER: US 09/547,276
 PRIOR FILING DATE: 2000-04-11
 PRIOR APPLICATION NUMBER: US 60/196,267
 PRIOR FILING DATE: 2000-04-11
 PRIOR APPLICATION NUMBER: US 60/196,460
 PRIOR FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: US 60/196,527
 PRIOR FILING DATE: 2000-04-11
 PRIOR APPLICATION NUMBER: US 60/196,528
 PRIOR FILING DATE: 2000-04-11
 PRIOR APPLICATION NUMBER: US 09/587,837
 PRIOR FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: US 60/240,503
 PRIOR FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: US 60/240,508
 PRIOR FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: US 60/240,539
 PRIOR FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: US 60/240,543
 PRIOR FILING DATE: 2000-10-13
 NUMBER OF SEQ ID NOS: 153
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 67
 LENGTH: 50
 TYPE: DNA

ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence : Exon 11
 US-09-736-969A-67

Query Match 3.0%; Score 20; DB 9; Length 50;
 Best Local Similarity 7.4e+04%; Pred. No. 0;
 Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 510 GCTCCCTGCCAGCGGCTCTGATGAGCTGAAGC 545
 Db 44 GCTCCCGAGCTGATGATGCTGAGCGCATC 9

RESULT 3
 US-10-131-827-3541
 Sequence 3541, Application US/10131827
 Publication No. US20040009479A1
 GENERAL INFORMATION:
 APPLICANT: Wohlgemuth, Jay
 ATTORNEY OR AGENT: FRY, Kirk
 ATTORNEY OR AGENT: Woodward, Robert
 ATTORNEY OR AGENT: Ly, Ngoc
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE DISEASES
 FILE REFERENCE: 506612000120
 CURRENT APPLICATION NUMBER: US/10/131,827
 CURRENT FILING DATE: 2002-09-05
 PRIOR APPLICATION NUMBER: US 10/006,290
 PRIOR FILING DATE: 2001-10-22
 PRIOR APPLICATION NUMBER: US 60/296,764
 PRIOR FILING DATE: 2001-06-08
 NUMBER OF SEQ ID NOS: 9090
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 3541

Query Match 3.0%; Score 20; DB 15; Length 50;
 Best Local Similarity 8.2%; Pred. No. 7.4e+04%;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 439 GGCTGGTGGCCAGTTGTGACTT 466
 Db 22 GGCTGGTCCAGAAATGTGTGCCATT 49

RESULT 4
 US-09-974-026-61/c
 Sequence 61, Application US/0974026
 Publication No. US20030194398A1
 GENERAL INFORMATION:
 APPLICANT: Tamburini, Paul P
 ATTORNEY OR AGENT: Davis, Gary
 ATTORNEY OR AGENT: Delaria, Katherine A
 ATTORNEY OR AGENT: Christopher, Mario R
 ATTORNEY OR AGENT: Daniel, Muller K
 TITLE OF INVENTION: Human Birunin
 FILE REFERENCE: 96-223-22
 CURRENT APPLICATION NUMBER: US/09/974,026
 CURRENT FILING DATE: 2001-10-10
 PRIOR APPLICATION NUMBER: US 09/144,428
 PRIOR FILING DATE: 1998-08-31
 PRIOR APPLICATION NUMBER: PCT/US97/03894
 PRIOR FILING DATE: 1997-03-10
 PRIOR APPLICATION NUMBER: US 08/725,251
 PRIOR FILING DATE: 1996-10-04
 PRIOR APPLICATION NUMBER: US 60/019,793
 PRIOR FILING DATE: 1996-06-14
 PRIOR APPLICATION NUMBER: US 60/013,106
 PRIOR APPLICATION NUMBER: US 60/013,106

PRIOR FILING DATE: 1996-03-11
 NUMBER OF SEQ ID NOS: 105
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 61
 LENGTH: 45
 TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Oligonucleotide used in in vitro mutagenesis in Example 9.

FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

RESULT 5
 US-09-780-53A-5931
 Sequence 531, Application US/09780533A
 PUBLICATION NO. US20030060611A1
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ATTORNEY: Blatt, Larry
 APPLICANT: McSwigan, Jim
 APPLICANT: Chowri, Bharat
 APPLICANT: Haebler, Pete
 TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 FILE REFERENCE: MBH00,878-A (400/011)
 CURRENT APPLICATION NUMBER: US/09/780,533A
 CURRENT FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: US 60/181,797
 PRIOR FILING DATE: 2000-02-11
 NUMBER OF SEQ ID NOS: 6679
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 5931
 LENGTH: 48
 TYPE: RNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

Query Match 2.9%; Score 19.6; DB 10; Length 48;
 Best Local Similarity 52.4%; Pred. No. 9.5e+04;
 Matches 22; Conservative 14; Indels 0; Gaps 0;

Qy 167 GTCAAGCAGCTGAAAGGAGCTGCCAGACG 200
 Db 36 GTGGCCATCTGCHGGCAGGTCAGCGAGCG 3

RESULT 7
 US-09-753-436-67/c
 Sequence 67, Application US/097534336
 Patent No. US200002933A1
 GENERAL INFORMATION:
 APPLICANT: Galilatin, W. Michael
 APPLICANT: Vazeux, Rosemary
 TITLE OF INVENTION: ICM-Related Materials and Methods
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Burin
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/753,436
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/382,289
 FILING DATE:
 APPLICATION NUMBER: US 08/487,113
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,754
 FILING DATE: 05-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/102,852
 FILING DATE: 05-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/009,266
 FILING DATE: 22-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/894,061
 FILING DATE: 05-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/889,724
 FILING DATE: 26-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,689
 FILING DATE: 27-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams, Joseph A., Jr.
 REGISTRATION NUMBER: 38,659
 REFERENCE/DOCKET NUMBER: 33282
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEX: (312) 474-0448
 TELEFAX: 25-3856

NUMBER OF SEQ ID NOS: 9090
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 4141
 LENGTH: 50
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-131-827-4141
 Query Match 2.9%; Score 19.6; DB 15; Length 50;
 Best Local Similarity 73.5%; Pred. No. 9.5e-04;
 Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 146 AGAAACTTGTGAAGTTGGTCAAGCAGCTGC 179
 Db 42 AGAAATTGTGGTTAGCTCTCGAGGCCGC 9
 RESULT 7
 Sequence 67, Application US/097534336
 Patent No. US200002933A1
 GENERAL INFORMATION:
 APPLICANT: Galilatin, W. Michael
 APPLICANT: Vazeux, Rosemary
 TITLE OF INVENTION: ICM-Related Materials and Methods
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Burin
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/753,436
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/382,289
 FILING DATE:
 APPLICATION NUMBER: US 08/487,113
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,754
 FILING DATE: 05-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/102,852
 FILING DATE: 05-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/009,266
 FILING DATE: 22-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/894,061
 FILING DATE: 05-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/889,724
 FILING DATE: 26-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,689
 FILING DATE: 27-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams, Joseph A., Jr.
 REGISTRATION NUMBER: 38,659
 REFERENCE/DOCKET NUMBER: 33282
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:
 LENGTH: 48 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-09-753-436-67

Query Match 2.9%; Score 19.4; DB 9; Length 48;
 Best Local Similarity 64.4%; Pred. No. 1.1e+05;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  271 CACACTCTCCGGAGGCCCTCGTGCACGCCAACAGCTGAA 315
Db   45 CAGACTGTCTGAGTTGACCTGGACTGGAACCTGGACCTGGCGCAA 1

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RESULT 8
 US-10-156-306-7723
 Publication No. US20030119017A1
 GENERAL INFORMATION: Application US/10156306
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 McSwiggen, James
 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
 to Inflammation: Levels of IKK-Gamma and PKR
 FILE REFERENCE: MBHB01-664-A (400/050)
 CURRENT APPLICATION NUMBER: US/10/156,306
 CURRENT FILING DATE: 2002-05-28
 NUMBER OF SEQ ID NOS: 8013
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 7723
 LENGTH: 48
 TYPE: RNA
 FEATURE: ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-10-156-306-7723

Query Match 2.9%; Score 19.4; DB 14; Length 48;
 Best Local Similarity 62.1%; Pred. No. 1.1e+05;
 Matches 18; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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Qy  324 CCTTCAGGACCAAGCTCCAGGAGCTCTGC 352
Db   20 CCUCUAGGACAUUGCUUAGCUCUG 48

```

RESULT 9
 US-10-163-942-67/C
 Sequence 67, Application US/10163942
 Publication No. US20030199423A1
 GENERAL INFORMATION:
 APPLICANT: Gallatin, W Michael
 Vazeur, Rosemary
 TITLE OF INVENTION: ICAM-Related Materials and Methods
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/163,942
 FILING DATE: 05-Jun-2002

RESULT 10
 US-09-874-547-6
 Sequence 6, Application US/09874547
 Patent No. US20020058269A1
 GENERAL INFORMATION:
 APPLICANT: No. US20020058269A1, Steffen
 APPLICANT: Kassner, Paul D.
 APPLICANT: Zymox, Inc.
 TITLE OF INVENTION: Screening of Phage Displayed Peptides
 TITLE OF INVENTION: Without Clearing of the Cell Culture
 FILE REFERENCE: 020144-001110US
 CURRENT APPLICATION NUMBER: US/09/874,547
 CURRENT FILING DATE: 2001-06-04
 PRIOR APPLICATION NUMBER: 60/209,503
 PRIOR FILING DATE: 2000-06-05
 NUMBER OF SEQ ID NOS: 84
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 6
 LENGTH: 50
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Primers for ScFv and Fab library generation (Table
 I) - MHC-Back3
 OTHER INFORMATION: I) - MHC-Back3
 US-09-874-547-6

Query Match 2.9%; Score 19.4; DB 9; Length 50;
 Best Local Similarity 70.3%; Pred. No. 1.1e+05;
 Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 513 CCCGTGAGCCGAGCTGCCATGCAAGCTTTC 549
 Db 14 CCCGCCGCATGCCCAAGTCAGCTGAGAGTC 50

RESULT 13
 US-10-219-195-45/c
 Sequence 45, Application US/10219195
 Publication No. US20030165917A1
 GENERAL INFORMATION:
 APPLICANT: ULLMAN, EDWIN
 APPLICANT: WU, MING PING
 APPLICANT: LIU, YEN PING
 TITLE OF INVENTION: ISOTHERMAL AMPLIFICATION IN NUCLEIC ACID ANALYSIS
 CURRENT APPLICATION NUMBER: US/10/219,195
 CURRENT FILING DATE: 2002-08-14
 PRIOR APPLICATION NUMBER: 60/312,505
 PRIOR FILING DATE: 2001-06-14
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 45
 LENGTH: 46
 TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Oligonucleotide
 US-10-219-195-45

Query Match 2.9%; Score 19.2; DB 14; Length 46;
 Best Local Similarity 67.5%; Pred. No. 1.2e+05;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 591 TCCAGGAGTGGGTACAGCGTGGCCCTGGTCTAAAGGA 630
 Db 46 TCAAGGAGAAGCTGNGCTACGTCGCCCTGGACTTGAGGA 7

RESULT 14
 US-09-740-668A-57/c
 Sequence 57, Application US/09740668A
 Patent No. US20020076700A1
 GENERAL INFORMATION:
 APPLICANT: Shimbek, Richard
 APPLICANT: Wohlgemuth, Jay
 APPLICANT: Woodward, Robert
 APPLICANT: LY, Ngoc
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE DISEASES
 FILE REFERENCE: 506612000120
 CURRENT APPLICATION NUMBER: US/10/131,827
 CURRENT FILING DATE: 2002-09-06
 PRIOR APPLICATION NUMBER: US 10/006,290
 PRIOR FILING DATE: 2001-10-22
 PRIOR APPLICATION NUMBER: US 60/296,764
 PRIOR FILING DATE: 2001-06-08
 NUMBER OF SEQ ID NOS: 9090
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 6776
 LENGTH: 50
 TYPE: DNA
 ORGANISM: Homo sapiens
 OTHER INFORMATION: US-10-131-627-6776

Query Match 2.9%; Score 19.2; DB 15; Length 50;
 Best Local Similarity 87.5%; Pred. No. 1.2e+05;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 221 AGGCCAACCTGCCAGGAGCAGTGT 247

Db 36 AGCGTGGAGCTGCTGAGGAAGCTG 1.0

RESULT 15
US-10-429-849-12/C

; Sequence 12, Application US/10429849

; PUBLIC INFORMATION:

; APPLICANT: TATSUKA, MASAAKI

; TITLE OF INVENTION: CELL CYCLE-REGULATING PROTEINS

; FILE REFERENCE: 05049/0102

; CURRENT APPLICATION NUMBER: US/10/429,849

; CURRENT FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: US/09/485,534

; PRIOR FILING DATE: 2000-02-14

; PRIOR APPLICATION NUMBER: PCT/JP98/03641

; PRIOR FILING DATE: 1998-08-17

; PRIOR APPLICATION NUMBER: 235371/1997

; PRIOR FILING DATE: 1997-08-15

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 12

; LENGTH: 38

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: Feature: Description of Artificial Sequence: Primer

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-10-429-849-12

Query Match Score 19; DB 12; Length 38;

Best Local Similarity 71.4%; Pred. No. 1.4e-05;

Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 287 GGCCTCGTCAGCCGCCACAGCTGAAGCTGA 321

Db 38 GGGGGCGCTGCGCCCGCTGCCCCCTAGCTGA 4

Search completed: February 29, 2004, 14:51:52
Job time : 271.199 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
C 1	23	3.4	48	3	US-08-828-533-37		Sequence 37, Appl
C 2	23	3.4	48	4	US-09-772-155-37		Sequence 37, Appl
C 3	19.8	2.9	45	1	US-0-176-412-5		Sequence 5, Appl
C 4	19.8	2.9	45	2	US-0-555-262A-5		Sequence 5, Appl
C 5	19.8	2.9	45	2	US-08-495-693B-5		Sequence 5, Appl
C 6	19.8	2.9	45	5	PCT-US94-14146-5		Sequence 5, Appl
C 7	19.6	2.9	45	4	US-19-144-428-61		Sequence 61, Appl
C 8	19.6	2.9	46	2	US-08-448-418-10		Sequence 10, Appl
C 9	19.6	2.9	46	4	US-09-146-979-10		Sequence 10, Appl
C 10	19.4	2.9	29	3	US-0-297-395-45		Sequence 45, Appl
C 11	19.4	2.9	48	1	US-08-412-882-67		Sequence 67, Appl
C 12	19.4	2.9	48	1	US-08-413-389-67		Sequence 67, Appl
C 13	19.4	2.9	48	2	US-08-487-113D-67		Sequence 67, Appl
C 14	19.4	2.9	48	2	US-08-413-503-67		Sequence 67, Appl
C 15	19.4	2.9	48	2	US-08-483-932-67		Sequence 67, Appl
C 16	19.4	2.9	48	2	US-0-720-422A-67		Sequence 67, Appl
C 17	19.4	2.9	48	3	US-08-714-017-67		Sequence 67, Appl
C 18	19.4	2.9	48	3	US-08-475-680-67		Sequence 67, Appl
C 19	19.4	2.9	50	4	US-09-874-547-6		Sequence 6, Appl
C 20	19	2.8	33	1	US-08-438-639-30		Sequence 30, Appl
C 21	19	2.8	33	1	US-07-813-33PA-30		Sequence 30, Appl
C 22	19	2.8	33	3	US-08-441-971-105		Sequence 105, App
C 23	19	2.8	33	3	US-0-221-653-105		Sequence 105, App
C 24	19	2.8	33	3	US-08-442-144A-105		Sequence 105, App
C 25	19	2.8	33	3	US-08-441-970-105		Sequence 105, App
C 26	19	2.8	45	5	PCT-US94-14106-18		Sequence 18, Appl
C 27	18.8	2.8	36	1	US-08-624-545-16		Sequence 16, Appl

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GenCore version 5.1.6
OM nucleic - nucleic search, using SW model
Run on: February 29, 2004, 11:48:29 ; Search time 68.0506 Seconds
Title: US-09-904-568-3_COPY_294_966
Perfect score: 673
Sequence: 1 aatgtctgttgtggggctg.....gtcgagcgcagactgcaggac 673
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 682709 seqs, 277475446 residues
Total number of hits satisfying chosen parameters: 839752

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Listing First 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/pctodata/2/ina/5A COMB.seq:
2: /cgn2_6/pctodata/2/ina/5B COMB.seq:
3: /cgn2_6/pctodata/2/ina/6A COMB.seq:
4: /cgn2_6/pctodata/2/ina/6B COMB.seq:
5: /cgn2_6/pctodata/2/ina/PCTMS COMB.seq:
6: /cgn2_6/pctodata/2/ina/backfiles1.seq:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
US-08-828-533-37/c
; Sequence 37, Application US/08828533
; Patent No. 6180319
; GENERAL INFORMATION:
; APPLICANT: Ruderman, Joan V.
; APPLICANT: Hershko, Avram
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Townsley, Fiona
; APPLICANT: Aristarkov, Alexander
; APPLICANT: Bytan, Esther
; APPLICANT: Yu, Hongtao
; TITLE OF INVENTION: NOVEL CYCLIN-SELECTIVE UBIQUITIN CARRIER
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; ZIP: 02109
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; COMPUTER TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828-533
; FILING DATE: 31-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ph.D., Ann-Louise
; REGISTRATION NUMBER: 33-123
; REFERENCE/DOCKET NUMBER: HAZ-015C1P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)526-6000
; TELEX/FAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base Pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FRAGMENT TYPE: linear
; Query Match Score 23 ; DB 3 ; Length 48 ;
; Best Local Similarity 83.9% ; Pred. No. 5.8e+3 ;
; US-08-828-533-37

Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

APPLICANT: Bard, Jonathan A.
WALKER, Mary

APPLICANT: Branchek, Theresa

APPLICANT: Weinshank, Richard L.

TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE

TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE

TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEES: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

CONTY: U.S.A.

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,412

FILING DATE:

CLASIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 2B,678

REFERENCE/DOCKET NUMBER: 4443/JFW/TEP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: 42523 COOP UI

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 45 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-176,412-5

Query Match 2.9%; Score 19.6; DB 1; Length 45;

Best Local Similarity 69.2%; Pred. No. 3, 3e+04;

Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 131 GACAGGAGCACGTTGAAAGTGTGCTGAGTTGTGGTC 169

Db 44 GAGAGTTGCGATGAGATGTTGACATTCTAC 6

RESULT 4

US-08-555-268A-5/c

Sequence 5, Application US/08555268A

Patent No. 5958709

GENERAL INFORMATION:

APPLICANT: Bard, Jonathan A.

APPLICANT: Branchek, Theresa

APPLICANT: Weinshank, Richard L.

TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE

TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE

TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEES: Cooper & Dunham LLP

STREET: 1115 Avenue of the Americas

CITY: New York

STATE: New York

CONTY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

RESULT 1

US-08-176-412-5/c

Sequence 5, Application US/08176412

Patent No. 5516653

GENERAL INFORMATION:

Qy 304 CACAGGCTGAAGCCCTGACACCTTCAGGAC 334

Db 47 CACAGGCTGAAGCCCAACCTACAGGTAC 17

RESULT 3

US-08-176-412-5/c

Sequence 5, Application US/08176412

Patent No. 5516653

GENERAL INFORMATION:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/555, 268A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28 678
 REFERENCE/DOCKET NUMBER: 44 743-Z/JPN/MAT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEX/FAX: (212) 391-0526
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-555-268A-5

Query Match Score 2.9%; DB 2; Length 45;
 Best Local Similarity 69.2%; Pred. No. 3.3e+04;
 Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 131 GACAGGAGCACGTTCAAAAGTTCTGAGATTGTGGTC 169
 Db 44 GAGAGTTTACGATCAGATGTTGAGATTCCTCATC 6

RESULT 6
 PCT-US94-14436-5/c
 Sequence 5, Application PC/TUS9414436
 GENERAL INFORMATION:
 APPLICANT: Bard, Jonathan A.
 APPLICANT: Walker, Mary
 APPLICANT: Branchek, Theresa
 APPLICANT: Weinschank, Richard L.
 TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
 Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14436
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28 678
 REFERENCE/DOCKET NUMBER: 44 743-A-PCT\JPN\MAT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 PCT-US94-14436-5

Query Match Score 2.9%; DB 5; Length 45;
 Best Local Similarity 69.2%; Pred. No. 3.3e+04;
 Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 131 GACAGGAGCACGTTCAAAAGTTCTGAGATTGTGGTC 169
 Db 44 GAGAGTTTACGATCAGATGTTGAGATTCCTCATC 6

RESULT 7
 US-09-144-428-61/c
 Sequence 61, Application US/09144428
 Patent No. 6583108
 GENERAL INFORMATION:
 APPLICANT: BAYER CORPORATION, The
 APPLICANT: TAMBURINI, Paul P
 APPLICANT: DAVIS, Gary
 APPLICANT: DELARA, Katherine A
 APPLICANT: MARLIER, Christopher W
 APPLICANT: MULLER, Daniel K
 TITLE OF INVENTION: HUMAN BIKONIN
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McDonnell Boehnen Hulbert & Bergoff
 STREET: 300 S. Wacker Drive Suite 3200
 CITY: CHICAGO
 STATE: ILLINOIS
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/144,428
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/03894
 FILING DATE: 10-MAR-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/013,106
 FILING DATE: 11-MAR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/019,793
 FILING DATE: 14-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/725,251
 FILING DATE: 04-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: CHAO, Mark
 REGISTRATION NUMBER: 37,293
 REFERENCE/DOCKET NUMBER: 96,223-II
 TELEPHONE: (312) 913-0001
 TELEFAX: (311) 913-0002
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: not relevant
 MOLECULE TYPE: DNA (genomic)
 US-09-144-428-61

Query Match 2.9%; Score 19.6; DB 4; Length 45;
 Best Local Similarity 73.5%; Pred. No. 3.7e+04;
 Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 167 GTCAAGAGCCCTGAGGGAGACTGCCGAGCG 200
 Db 36 GTGCGCCTGCGGGCGAGTCAGCTGAG 3

APPLICANT: Griffiths, Andrew D
 APPLICANT: Hoogenboom, Hendricus RJM
 APPLICANT: Malmqvist, Magnus
 APPLICANT: Marks, James D
 APPLICANT: McGuiness, Brian T
 APPLICANT: Pope, Anthony R
 APPLICANT: Prospero, Terence D
 APPLICANT: Winter, Gregory P
 TITLE OF INVENTION: Multivalent and Multispecific Binding Proteins, Their Manufacture and Use
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall O'Toole Gerstein Murray and Burin
 STREET: 6310 Sears Tower 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/448,418
 FILING DATE: 14-MAY-1996
 CLASSIFICATION: 435
 CLASSIFICATION: C12N 15/62, 15/70, C07K 1/00
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB93/02492
 FILING DATE: 03-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9225453.1
 FILING DATE: 04-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9300816.7
 FILING DATE: 16-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 93303614.7
 FILING DATE: 10-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9319969.3
 FILING DATE: 22-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 28111/32651
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 46 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA primer
 US-08-448-18-10

RESULT 9
 US-09-146-919-10
 Sequence 10, Application US/09146979
 Patent No. 6491123
 GENERAL INFORMATION:
 APPLICANT: Holliger, Kaspar-Philipp
 APPLICANT: Griffiths, Andrew D
 APPLICANT: Hoogenboom, Hendricus RJM
 APPLICANT: Malmqvist, Magnus

APPLICANT: Marks, James D
 APPLICANT: McGuinness, Brian T
 APPLICANT: Pope, Anthony R
 APPLICANT: Probert, Terence D
 APPLICANT: Winter, Gregory P
 TITLE OF INVENTION: Multivalent and Multispecific Binding Proteins, Their Manufacture and Use
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall O'Toole Gersstein Murray and Borun
 STREET: 6300 Sears Tower 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/146,979
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/448,418
 FILING DATE: 14-MAY-1996
 APPLICATION NUMBER: PCT/GB93/02492
 PILING DATE: 03-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9225453.1
 FILING DATE: 04-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9300816.7
 FILING DATE: 16-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 93303614.7
 FILING DATE: 10-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 93119969.3
 FILING DATE: 22-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 46 base pairs
 TYPE: nucleic acid
 STRANDBNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA primer
 US 09-146-979-10

Query Match 2.9%; Score 19.6; DB 4; Length 46;
 Best Local Similarity 66.7%; Pred. No. 3.7e+04;
 Matches 28; Conservative 14; Indels 0; Gaps 0;

Qy 510 GCTGCGTGGAGGCCAGGCTTATGACCTGAGCTTCAG 551
 Db 4 GCGGCCAGCCGGCATGCCAGGTGAGGACTAG 45

RESULT 10
 US 08-297-395-45/C
 Sequence 45, Application US/08297395A
 GENERAL INFORMATION:
 APPLICANT: Howard L. Weiner
 ATTORNEY/AGENT INFORMATION:
 NAME: David A. Hafner
 TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT EPITOPES OF MYELIN BASIC PROTEIN
 FILE REFERENCE: 1010/05723US3

CURRENT APPLICATION NUMBER: US/08/297-395A
 CURRENT FILING DATE: 1994-08-11
 EARLIER APPLICATION NUMBER: 08/059,189
 EARLIER FILING DATE: 1993-05-16
 EARLIER APPLICATION NUMBER: 07/502,559
 EARLIER FILING DATE: 1990-03-30
 EARLIER APPLICATION NUMBER: PCT/US88/02139
 EARLIER FILING DATE: 1988-06-24
 EARLIER APPLICATION NUMBER: 07/065,734
 EARLIER FILING DATE: 1987-06-24
 NUMBER OF SEQ ID NOS: 84
 SOFTWARE: Fast-SEQ for Windows Version 3.0
 SEQ ID NO: 45
 LENGTH: 29
 TYPE: DNA
 ORGANISM: Homo sapiens
 US -08-297-395-45

Query Match 2.9%; Score 19.4; DB 3; Length 29;
 Best Local Similarity 79.3%; Pred. No. 3.7e+04;
 Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 422 GTGCCAGCAGGAGGGAGCCGGCTCTGC 450
 Db 29 GTGCTTACCAAGAGGAGCTCTGC 1

RESULT 11
 US-08-482-882-67/C
 Sequence 67, Application US/08482882
 Patent No. 5773218
 GENERAL INFORMATION:
 APPLICANT: Gallatin, W. Michael
 APPLICANT: Vazeux, Rosemary
 TITLE OF INVENTION: ICAM-Related Materials and Methods
 NUMBER OF SEQUENCES: 116
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gersstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,882
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,754
 FILING DATE: 26-MAY-1992
 PRIORITY APPLICATION NUMBER: US 08/102,852
 FILING DATE: 05-AUG-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/009,266
 FILING DATE: 22-JUN-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/894,061
 FILING DATE: 05-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/889,724
 FILING DATE: 26-MAY-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,689
 FILING DATE: 27-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 573218and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 32178

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 SEQUENCE FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 48 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US - 08-483-389-67

Query Match 2.9%; Score 19.4; DB 1; Length 48;
 Best Local Similarity 64.4%; Pred. No. 4.2e-04;
 Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 271 CACACTGCTCCAGCAGGCCCTCGGTCTGCCCTCACAGCCTGAA 315
 Db 45 CAGACTGCTGCAAGTGCACCTGGACTGGACACTGGACTGGACACCTGGCTGAA 1

RESULT 13
 US-08-487-113D-67/C
 ; Sequence 67, Application US/08487113D
 ; Patent No. 5837822
 ; GENERAL INFORMATION:
 ; APPLICANT: Vazeux, Rosemary W. Michael
 ; TITLE OF INVENTION: ICAM-Related Materials and Methods
 ; NUMBER OF SEQUENCES: 120
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patenter Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,113D
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/286,754
 ; FILING DATE: 05-AUG-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/102,852
 ; FILING DATE: 05-AUG-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/009,266
 ; FILING DATE: 22-JAN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/102,952
 ; FILING DATE: 05-AUG-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/009,266
 ; FILING DATE: 22-JAN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/894,061
 ; FILING DATE: 05-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/889,724
 ; FILING DATE: 26-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,689
 ; FILING DATE: 27-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Suh, Young J.
 ; REGISTRATION NUMBER: P-41,337
 ; REFERENCE/DOCKET NUMBER: 2-86/322760
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-6600
 ; INFORMATION FOR SEQ ID NO: 67:
 ; LENGTH: 48 base pairs
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: nucleic acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA

US-08-487-113D-67

Query Match 2.9%; Score 19.4; DB 2; Length 48;
 Best Local Similarity 64.4%; Pred. No. 4.2e+04;
 Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 271 CACACTGCTCCAGCAGGCCCTCGGTGCCCCACAGGCTGAA 315
 Db 45 CAGACTGCTGCACTGGACTTGACACTGGACACCTGGCCGCAA 1

RESULT 15
 US-08-483-932-67/C
 ; Sequence 67, Application US/08483932

GENERAL INFORMATION:
 / Sequence 67, Application US/08483932
 / PATENT NO.: 5869262
 / APPLICANT: Gallatin, W. Michael
 / ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
 / TITLE OF INVENTION: ICAM-Related Materials and Methods
 / NUMBER OF SEQUENCES: 116
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 / STREET: 6300 Sears Tower, 233 S. Wacker Drive
 / CITY: Chicago
 / STATE: Illinois
 / COUNTRY: USA
 / ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/473,503
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/286,754
 FILING DATE: 05-AUG-1994
 APPLICATION NUMBER: US 08/102,852
 FILING DATE: 05-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/009,266
 FILING DATE: 22-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/894,061
 FILING DATE: 05-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/889,724
 FILING DATE: 26-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,689
 FILING DATE: 27-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5869262and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 32178
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 48 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-483-932-67

Query Match 2.9%; Score 19.4; DB 2; Length 48;
 Best Local Similarity 64.4%; Pred. No. 4.2e+04;
 Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 271 CACACTGCTCCAGCAGGCCCTCGGTGCCCCACAGGCTGAA 315
 Db 45 CAGACTGCTGCACTGGACTTGACACTGGACACCTGGCCGCAA 1

Mon Mar 1 10:00:10 2004

us-09-904-568-3_copy_294_966_sz1m50.rni

Page 8

Search completed: February 29, 2004, 14:42:41
Job time : 70.0506 secs

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OM nucleic - nucleic search, using SW model

Run on: February 29, 2004, 10:34:43 ; Search time 2034.51 Seconds

(without alignments)
98.7168 Million cell updates/sec

Perfect score: US-09-904-568-3_COPY_294_966

Sequence: 1 aatctgtgtggggctg.....gttagcgagactgcaggac 673

Scoring table: IDENTITY_NTC
Gapext 1.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters:

138346

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Minimum DB seq length: 0

Maximum DB seq length: 50

Database : EST:*

1: em_estba:*

2: em_estbum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_espd1:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hrc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_fum:*

18: em_gss_irv:*

19: em_gss_pnn:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rnd:*

26: em_gss_prg:*

27: em_gss_vrl:*

28: gb_gssi:*

29: gb_gss1:*

RESULTS

RESULT 1

AU102670/c LOCUS AU102670 Sugano Homo sapiens mRNA library Homo sapiens cDNA clone

DEFINITION CAS07213, mRNA sequence.

ACCESSION AU102670.1 VERSION EST.

KEYWORDS SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Mammalia; Primates; Catarrhini; Homidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE AUTHORS Hata,H., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakai,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBL Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

PUBMED 11375929

COMMENT Contact: Yutaka Suzuki

Department of Virology Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-0039, Japan
Email: yutsuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and

SUMMARIES

%

Result No.	Score	Query Length	DB ID	Description
C 1	21.8	3.2	50 9 AU102670	AU102670
C 2	20.8	3.1	50 9 AL946896	AL946896 Arabidops
C 3	20.6	3.1	45 12 BG772081	BG772081 602721525
C 4	20	3.0	46 14 H45385	H45385 yn99c12.r1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES SOURCE Location/Qualifiers 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CAGT213"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN Query Match 3..24; Score 21.8; DB 9; Length 50;
 Best Local Similarity 65.3%; Pred. No. 1e+06;
 Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

RESULT 3
 AL946896 50 bp DNA linear GSS 24-OCT-2002
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence Gk-299G11-015556,
 Genomic survey sequence.

ACCESSION AL946896
 VERSION AL946896..1 GI:24403518
 KEYWORDS GSS;
 ORGANISM Arabidopsis thaliana (thale cress)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 Strizhov, N., Li, Y., Rosso, M., Viohoever, P., Dekker, K., Saedler, H.
 AUTHORS and Weisshaar, B.
 TITLE A pipeline for automated high-throughput generation of ESTs
 (flanking sequence tags) from Arabidopsis thaliana T-DNA
 transformed lines
 Unpublished

REFERENCE 2 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
 AUTHORS for flanking sequence tag based reverse genetics
 JOURNAL Unpublished

REFERENCE 3 (bases 1 to 50)
 AUTHORS Li, Y., Strizhov, N., Rosso, M. and Weisshaar, B.
 JOURNAL Direct Submission
 COMMENT This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At1g67400. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES SOURCE
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GR299G11-015556"
 /note="PCR was performed on DNA from Arabidopsis thaliana Plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment (8) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were

processed for submission. T-DNA derived sequences were removed."

ORIGIN Query Match 3..18; Score 20.8; DB 29; Length 50;
 Best Local Similarity 70.0%; Pred. No. 1..6e+06;
 Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

RESULT 4
 QY 595 GGAGCTGGGTACAGCGTGGCCCTGGGCTAAAGGAGATG 634
 Db 41 GGATCTGCTTTCTGGTGCCCTTGCTGTTATGGACAG 2

ORIGIN Query Match 3..24; Score 21.8; DB 9; Length 50;
 Best Local Similarity 65.3%; Pred. No. 1e+06;
 Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 DEFINITION EST 15-MAY-2001
 LOCUS BG772081/c mRNA sapiens cDNA clone IMAGE:4838287 5',
 mRNA sequence.

ACCESSION BG772081..1 GI:14082734
 VERSION EST.
 KEYWORDS SOURCE : Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 45)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 Email: cspbs@rmall.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM10722 row: a column: 08
 High quality sequence stop: 45.
 FEATURES Location/Qualifiers 1..45
 SOURCE /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4838287"
 /lab_host="IDH10B"
 /clone_id="NIH_MGC_97"
 /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site: 1; Bath: SalI-XbaI (gtcsag); Oligo-dT primed using primer 5'-TTTTTTTTTNTVN-3', size-selected for average insert size 2.2 kb and normalized to Rot 5. This is a primary library enriched for full-length clones and constructed using the Captrappr method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC library."

ORIGIN Query Match 3..18; Score 20.6; DB 12; Length 45;
 Best Local Similarity 67.4%; Pred. No. 1..7e+06;
 Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

RESULT 4
 QY 275 CAGCTCAGGAGGCCCTGCGTGCCTCCACAGGCTGAAGC 317
 Db 44 CGCGCCACCCGCCCATGTCCCCCTCTGCTCCCGC 2

DEFINITION Y999c12.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:176566 5' similar to SP:TS2_MOUSE P10712 TRANSCRIPTION

FACTOR S-II , mRNA sequence.

ACCESSION H45385
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 46)

REFERENCE Hillier,L., Clark,N., Dubuge,T., Elliston,K., Hawkins,M., Holtzman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riffkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

AUTHORS The WashU-Merck EST Project.

TITLE Unpublished (1995)

JOURNAL Contact: Wilson RK

COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers 1..46

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GB:3838762"
/db_xref="Exon:9606"
/clone="IMAGE3:176566"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DRI0B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b5HB55Y"
/note="Organ: brain; Vector: pRT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTATCAACTCTGAGTGGCACGCCGGCGCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library went through one round of normalization to a COT = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

FEATURES source

ORIGIN

Query Match 3.0%; Score 20; DB 14; Length 46;
Best Local Similarity 72.2%; Pred. No. 2.3e+06;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

RESULT 6

AI153463

LOCUS uc53e11..rl Soares_thymus_2NbMT Mus musculus cDNA clone

DEFINITION IMAGE:1423985' similar to SW:PHLX_RABIT Q05017 PHOSPHOLIPASE A2 PRECURSOR ; mRNA sequence.

ACCESSION AI153463

VERSION 1

Query 351 GCATCCCGAACACCTGGGGACTTGCCAGCG 386

Db 41 GCTTCTTCAGGACTGTGAGACTGGCCAGTG 6

Query Match 2.9%; Score 19.8; DB 14; Length 45;
Best Local Similarity 77.4%; Pred. No. 2.5e+06;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 6

AI153463

LOCUS uc53e11..rl Soares_thymus_2NbMT Mus musculus cDNA clone

DEFINITION IMAGE:1423985' similar to SW:PHLX_RABIT Q05017 PHOSPHOLIPASE A2 PRECURSOR ; mRNA sequence.

ACCESSION AI153463

VERSION 1

Query 628 GGAGATGGAGATGGAAAGCTGTGAGTTGAGGTGGCAG 658

Db 1 GAAGATGGCTACTCTGGAGTTGAGGTGGCAG 31

KEYWORDS EST; Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognath; Muridae; Mus.

REFERENCE 1 (bases 1 to 46)

AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Weising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE Unpublished (1996)

JOURNAL Contact: Marra M/Mouse EST Project

COMMENT WASHU-HUMAN Mouse EST Project

Washington University School of Medicine P 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

TeL: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:913456

Seq Primer: -28ml3 rev2 ET from Amersham

Possible reversed clone: similarity on wrong strand

Trace considered overall poor quality

High quality sequence stop: 1.

FEATURES source

1. .46

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:1429388"

/sex="male"

/tissue_type="Thymus"

/dev_stage="4 weeks"

/lab_host="DH10B"

/clone_id="Soares_thymus_2NBMT"

/note="vector: PT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TTTACCAATTGAGTGGAGGCGCCGCTTTCCTTTTTTTT3'] double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bent Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 2.9% Score 19.8; DB 9; Length 46;

Best Local Similarity 69.2%; Pred. No. 2.6e+0; Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

DEFINITION ING1094, mRNA sequence.

ACCESSION AU102937

VERSION AU102937.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

KEYWORDS EST. Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognath; Muridae; Mus.

REFERENCE 1 (bases 1 to 46)

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Sugiyama, A., and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

COMMENT Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan

Email: yuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES source

1. .50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="ING1064"

/clone_id="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match Similarity 2.9%; Score 19.8; DB 9; Length 50;
 Best Local Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 268 GCACACACTGCTCAGAGGCCCTCGTGCCTGCCACAGCCCTGA 314
 Db 50 GCAAGCCGGCTGTGCGGCCACGCTTGCGCCCTAACCTCTGA 4

RESULT 9

AU106019/C LOCUS AU106019 Sugano Homo sapiens cDNA clone X1A1053, mRNA sequence.

ACCESSION AU106019 VERSION EST

KEYWORDS SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A., and Sugano, S.

TITLE Diverse transcript initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

PUBMED 11375929

COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
 Email: yszukie@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A., and Sugano, S. Construction and characterization of a full-length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES source

1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match Similarity 2.9%; Score 19.8; DB 9; Length 50;
 Best Local Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 236 GAGGGACCTGGTGGCTGTGGCACCATGACACATGCTCCA 282
 Db 50 GAGGCAAAGGGGGGAGGGAGGAAATACACAGCTCTA 4

RESULT 10

AL651763/C LOCUS AL651763 XbaI-gastrula Silurana tropicalis cDNA clone TGas036n06 5', mRNA sequence.

ACCESSION AL651763 VERSION AL651763.1

KEYWORDS SOURCE Silurana tropicalis (western clawed frog)

ORGANISM Silurana tropicalis

REFERENCE 1. (bases 1 to 50)
 Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.

AUTHORS

FEATURES source

1..40
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

Sanger Xenopus tropicalis EST project 2001 (11_2003)

Unpublished (2003)

Comment Contact: Huckle E

Sanger Institute
 Hinckton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk

This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn. cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end. Vector: pCS107, Site 1: EcoRI, Site 2: NotI

Sanger Xenopus tropicalis EST project 2001 (TROPICALIS_SEQUENCE_ID: TGas036n06_pkSP6 Sequencing primer: SF6)

Location/Qualifiers

1..50
 /organism="Silurana tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TGas036n06"
 /dev_bstage="gastrula (stages 10-5-12 mixed)"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-gastrula"
 /note=Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

ORIGIN

Query Match Similarity 2.9%; Score 19.6; DB 9; Length 50;
 Best Local Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 201 GTGTSCAGCTCTGGTCTGGCTAGGCCAACCTGGAGAGCTGGT 250
 Db 50 GTGCCCCCTATGGGACCTGCGACCTGGCCATCTGAGCTGGTT 1

RESULT 11

BI160469/C LOCUS BI160469 40 bp mRNA
 DEFINITION 6028643-2F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5018743 5', mRNA sequence.

ACCESSION BI160469 VERSION BI160469.1

KEYWORDS SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteridae; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 40)
 NIH-MGC http://mgc.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rabin Laboratory

CDNA Library Arrayed by: The T.M.A.G.E. Consortium (TMCN)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/TMCN at:
 http://image.llnl.gov

Plate: LLCH1832 row: P column: 08

High quality sequence stop: 40.

Location/Qualifiers

1..40
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

/clone="IMAGE:5018743"
 /tissue_type="epithelial carcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone.lib="NIH MGC 42"
 /note="Organ: Pancreas; Vector: pOTB7; Site 1: XbaI;
 Site 2: EcoRI; cDNA made by Oligo-dT Priming.
 Directionally cloned into EcoRI/XbaI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library. |"

ORIGIN

Query Match 2.9%; Score 19.2%; DB 29; Length 43;
 Best Local Similarity 67.5%; Pred. No. 3. 3e+06;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 229 CCTGCCGGAGGAGCACTGGTCCCTGCTGCAGGGATG 268
 Db 1 CCTGCCAGGAGCAGCAGATCTGAGCAGG 40

RESULT 13

CG708599 LOCUS CG708599 44 bp DNA linear GSS 20-OCT-2003
 DEFINITION 1119010A02.1IEL.x1 1119 - Rescuemu Grid AA Zea mays genomic, genomic
 survey sequence.

ACCESSION CG708599
 VERSION CG708599.1 GI:37734505
 KEYWORDS GSS,
 SOURCE zeamays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade: Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 44)

REFERENCE

AUTHORS Walbot, V.
 TITLE Maize genomic sequences found using engineered Rescuemu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot, V.
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Very probable ligation site of ends cut by single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1119037 row: 32

FEATURES

SOURCE

1. 44 /organism="Zea mays"
 /mol_type="Genomic DNA"
 /cultivar="mixed background W23/A-88/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone.lib="1119 - Rescuemu Grid AA"
 /note="Organ: Leaf; Vector: Rescuemu (engineered from
 PBBluescript backbone); Site 1: BamHI; Site 2: BglII;
 Rescuemu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcriptional
 units. For more information on Rescuemu, go to the web
 site 'www.zmdb.iastate.edu', and follow the links for
 'Rescuemu'. Grid AA was grown at UC San Diego in 2002. DNA
 was extracted from leaf strips, double digested using
 BamHI and BglII, and ligated to form circular plasmids.
 DH10B cells were transformed and then screened on LB
 plates with ampicillin."

ORIGIN

Query Match 2.9%; Score 19.2%; DB 29; Length 44;
 Best Local Similarity 67.5%; Pred. No. 3. 3e+06;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 229 CCTGCCGGAGGAGCACTGGTCCCTGCTGCAGGGATG 268
 Db 2 CCTGCCAGGAGCAGCAGATCTGAGCAGG 41

RESULT 14
 CG708605 CG708605 44 bp DNA linear GSS 20-OCT-2003
 LOCUS DEFINITION survey sequence - Rescuemu Grid AA Zea mays genomic, genomic
 SURVEY Sequence
 ACCESSION CG708605
 VERSION 1
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoideae; Andropogoneae; Zea.
 (bases 1 to 44)
 REFERENCE 1
 AUTHORS Walbot, V.
 TITLE Maize Genomic Sequences found using engineered Rescuemu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Very probable ligation site of ends cut by single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1119010 row: 33

FEATURES source
 1..44
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577",
 /tissue_type="leaf",
 /dev_stage="adult",
 /lab_host="DH10B",
 /clone_lib="1119 - Rescuemu Grid AA",
 /note="Organ: leaf; Vector: Rescuemu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BgIII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA units. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site www.zmdb.iastate.edu, and follow the links for Rescuemu. Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
 Query Match 2.9%; Score 19.2; DB 29; Length 44;
 Best Local Similarity 67.5%; Pred. No. 3.3e+06
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 229 CCTCGCGAGGAGCAGCTGGTCCCTGGCAGGATG 268
 Db 2 CCTGCAGAGGAGCAGCAGATCATCTGAGCGA2AGG 41

Search completed: February 29, 2004, 14:40:15
 Job time : 2037.51 secs

RESULT 15
 CG708611 CG708611 44 bp DNA linear GSS 20-OCT-2003
 LOCUS DEFINITION survey sequence - Rescuemu Grid AA Zea mays genomic, genomic
 SURVEY Sequence
 ACCESSION CG708611
 VERSION 1
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

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score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES						
	Result No.	Score	% Match	Length	DB ID	Description
OM nucleic - nucleic search, using sw model	C	1	23	3.4	48	6 AR127012 Sequence
Run on: February 29, 2004, 10:05:33 ; Search time 2729.03 Seconds	C	2	23	3.4	48	AR285578 Sequence
Perfect score: 673	C	3	21	3.1	45	6 A76101 Sequence 40
Sequence: 1 aatgtctgtctgtggggctg.....gtggcgccagactggaggac 673	C	4	20.6	3.1	40	6 AX517113 Sequence
Scoring table: IDENTITY_NUC	C	5	20.6	3.1	40	6 AX519642 Sequence
Gapop 11.0 , Gapext 1.0	C	6	20.2	3.0	42	6 B41550 Method for
Searched: 3470272 seqs, 2167151695 residues	C	7	20.2	3.0	42	6 BD013091 Method fo
Total number of hits satisfying chosen parameters:	1603530					
Minimum DB seq length: 0	C	8	20	3.0	50	5 CRKGDCG
Maximum DB seq length: 50	C	9	19.8	2.9	45	6 AX173088 Sequence
Post-processing: Minimum Match 0%	C	10	19.8	2.9	45	6 AR075912 Sequence
Maximum Match 100%	C	11	19.8	2.9	45	6 AR083198 Sequence
Listing first 45 summaries	C	12	19.8	2.9	45	6 BD247107 Improved
Database :	C	13	19.8	2.9	45	5 T20781 Sequence 5
GenEmbl:*	C	14	19.8	2.9	45	6 BD237452 Single nu
1: gb_ba:*	C	15	19.8	2.9	48	6 BD270516 Method. 7
2: gb_htg:*	C	16	19.8	2.9	48	6 AX026686 Sequence
3: gb_in:*	C	17	19.8	2.9	50	9 AF057510 Homo Bapi
4: gb_om:*	C	18	19.6	2.9	41	6 AX513948 Sequence
5: gb_ov:*	C	19	19.6	2.9	41	6 AX519287 Sequence
6: gb_dat:*	C	20	19.6	2.9	45	6 BD247648 A method
7: gb_Ph:*	C	21	19.6	2.9	45	6 AR345117 Sequence
8: gb_Pl:*	C	22	19.6	2.9	46	6 A38923 Sequence 10
9: gb_pr:*	C	23	19.6	2.9	46	6 AR054319 Sequence
10: gb_ro:*	C	24	19.6	2.9	46	6 AR265569 Sequence
11: gb_sts:*	C	25	19.6	2.9	48	6 AX221581 Sequence
12: gb_sy:*	C	26	19.4	2.9	31	6 E226067 Oligonucleo
13: gb_un:*	C	27	19.4	2.9	48	6 AR013871 Sequence
14: gb_vl:*	C	28	19.4	2.9	48	6 AR033825 Sequence
15: em_ba:*	C	29	19.4	2.9	48	6 AR042485 Sequence
16: em_fun:*	C	30	19.4	2.9	48	6 AR058365 Sequence
17: em_hum:*	C	31	19.4	2.9	48	6 AR088191 Sequence
18: em_in:*	C	32	19.4	2.9	48	6 BD237453 Single nu
19: em_mu:*	C	33	19.4	2.9	48	6 BD270517 Method. 7
20: em_om:*	C	34	19.4	2.9	48	6 AX026687 Sequence
21: em_or:*	C	35	19.4	2.9	48	6 AX583009 Sequence
22: em_ov:*	C	36	19.4	2.9	50	6 AX157594 Sequence
23: em_pat:*	C	37	19.4	2.9	50	6 AX351171 Sequence
24: em_ph:*	C	38	19.2	2.9	41	6 AX516097 Sequence
25: em_Pl:*	C	39	19.2	2.9	41	6 AX517503 Sequence
26: em_ro:*	C	40	19.2	2.9	45	6 AX840266 Sequence
27: em_sts:*	C	41	19	2.8	33	6 AR004376 Sequence
28: em_un:*	C	42	19	2.8	33	6 AR097167 Sequence
29: em_vl:*	C	43	19	2.8	33	6 AR130665 Sequence
30: em_htg_hum:*	C	44	19	2.8	33	6 AR172014 Sequence
31: em_htg_inv:*	C	45	19	2.8	33	6 I82851 Sequence 30
32: em_htg_other:*						
33: em_htg_mus:*						
34: em_htg_pln:*						
35: em_htg_rid:*						
36: em_htg_mam:*						
37: em_htg_vrt:*						
38: em_sy:*						
39: em_htgo_hum:*						
40: em_htgo_mus:*						
41: em_htgo_other:*						

ALIGNMENTS

RESULT 1	AR127012/c	LOCUS	48_bp	DNA	
		DEFINITION	Sequence 37 from patent US 6180379.		
		ACCESSION	AR127012		
		VERSION	AR127012.1	GI:14113605	
		KEYWORDS	Unknown.		
		SOURCE	Unclassified.		
		ORGANISM	1 (bases 1 to 48)		
			Ruderman, J.V., Hershko, A., Kirschner, M.W., Townsley, F.,		
			Aristarkov, A., Bytan, R., and Yu, H.		
			Cyclin-selective ubiquitin carrier polypeptides		
			Patent: US 6180379-A 30-JAN-2001;		
			JOURNAL		

Pred. No. is the number of results predicted by chance to have a

FEATURES Location/Qualifiers 1..48 /organism="unknown" /mol_type="unassigned DNA"

ORIGIN

Query Match Score 23; DB 6; Length 48;
Best Local Similarity 83.9%; Pred. No. 2.5e+06;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 304 CACCAAGCTGAAAGCCTGACACCTTCAGGGAC 334
Db 47 CACCAAGGAGGCCAACCTACAGGTAC 17

RESULT 2
AR285578/C LOCUS AR285578 Sequence 37 from Patent US 6528633.
DEFINITION Sequence 37 from Patent US 6528633.
ACCESSION AR285578
VERSION AR285578.1 GI:29723140
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 48)
AUTHORS Ruderman,J.V., Hershko,A., Kirschner,M.W., Townsley,F.,
Aristarkov,A., Eyran,E. and Yu,H.
TITLE Cyclin-selective ubiquitin carrier polypeptides
JOURNAL Patent: US 658633-A 37 04-MAR-2003;
FEATURES Location/Qualifiers 1..48
SOURCE /organism="unknown" /mol_type="unassigned DNA"

ORIGIN

Query Match Score 23; DB 6; Length 48;
Best Local Similarity 83.9%; Pred. No. 2.5e+06;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 304 CACCAAGCTGAAAGCCTGACACCTTCAGGGAC 334
Db 47 CACCAAGGAGGCCAACCTACAGGTAC 17

RESULT 3
A76101/C LOCUS A76101 Sequence 40 from Patent WO9320210.
DEFINITION Sequence 40 from Patent WO9320210.
ACCESSION A76101
VERSION A76101.1 GI:6088242
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 45)
AUTHORS Taylor,G. and Stott,E.J.
TITLE ANTIBODIES FOR TREATMENT AND PREVENTION OF RESPIRATORY SYNCYTIAL VIRUS INFECTION
JOURNAL Patent: WO 9302010-A 40 14-OCT-1993;
SCORGEN LTD (GB); TAYLOR GEPAIDINE (GB)
FEATURES Location/Qualifiers 1..45
SOURCE /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"

ORIGIN

Query Match Score 21; DB 6; Length 45;
Best Local Similarity 66.7%; Pred. No. 6.2e+06;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 42 CTGGTGTAGTAGCACAGTGCCGAGTGAATTCCTGGGGCCCAGC 86

FEATURES Location/Qualifiers 1..48 /organism="unknown" /mol_type="unassigned DNA"

ORIGIN

Query Match Score 23; DB 6; Length 48;
Best Local Similarity 83.9%; Pred. No. 2.5e+06;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 304 CACCAAGCTGAAAGCCTGACACCTTCAGGGAC 334
Db 47 CACCAAGGAGGCCAACCTACAGGTAC 17

RESULT 4
AX517113/C LOCUS AX517113 Sequence 3311 from Patent WO02052044.
DEFINITION Sequence 3311 from Patent WO02052044.
ACCESSION AX517113
VERSION AX517113.1 GI:23565449
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 Nakamura,Y., Sekine,A., Tida,A. and Saito,S.
AUTHORS Nakamura,Y., Sekine,A., Tida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 3311 04-JUL-2002;
Riken (JP)
FEATURES Location/Qualifiers 1..40
SOURCE /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

ORIGIN

Query Match Score 20.6; DB 6; Length 40;
Best Local Similarity 74.3%; Pred. No. 7.6e+06;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 133 CAGGGACAGTCAGAAAGTTGCTGAAAGTTGCTGG 167
Db 36 CAGGGACAGTCAGAAAGTTGCTGAAAGTTGCTGG 2

RESULT 5
AX519642/C LOCUS AX519642 Sequence 5840 from Patent WO02052044.
DEFINITION Sequence 5840 from Patent WO02052044.
ACCESSION AX519642
VERSION AX519642.1 GI:23569993
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 Nakamura,Y., Sekine,A., Tida,A. and Saito,S.
AUTHORS Nakamura,Y., Sekine,A., Tida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 5840 04-JUL-2002;
Riken (JP)
FEATURES Location/Qualifiers 1..40
SOURCE /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

ORIGIN

Query Match Score 20.6; DB 6; Length 40;
Best Local Similarity 74.3%; Pred. No. 7.6e+06;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 133 CAGGGACAGTCAGAAAGTTGCTGAAAGTTGCTGG 167
Db 36 CAGGGACAGTCAGAAAGTTGCTGAAAGTTGCTGG 2

RESULT 6
E41550/C LOCUS E41550
DEFINITION Method for yielding male abortive plants.
ACCESSION E41550

RESULT 8
 CERGDCC/c
 CHIKDCG
 Gallus gallus gene for glycine decarboxylase, partial cds.
 50 bp DNA linear VRT 17-DEC-2002

LOCUS CHIKDCG
 DEFINITION Gallus gallus gene for glycine decarboxylase, partial cds.
 ACCESSION D90240
 VERSION D90240.1 GI:222888
 KEYWORDS
 SOURCE
 ORGANISM Gallus gallus (chicken)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosanida; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallinae.
 REFERENCES
 AUTHORS Kume,A., Koyata,H., Sakakibara,T., Ishiguro,Y., Kure,S. and Hiraga,K.
 TITLE The glycine cleavage system. Molecular cloning of the chicken and human glycine decarboxylase cDNAs and some characteristics involved in the deduced protein structures
 JOURNAL J. Biol. Chem. 266 (5), 3323-3329 (1991)
 MEDLINE 91131643
 PUBMED 1993704
 COMMENT These data kindly submitted in computer readable form by: Koichi Hiraga
 DEPARTMENT Department of Biochemistry
 Toyama Medical and Pharmaceutical University
 SCHOOL School of Medicine
 ADDRESS 2630 Sugitani, Toyama
 CITY Toyama
 STATE 930-01
 ZIP
 COUNTRY Japan
 PHONE 81-764-34-2281 x2330
 FAX 81-764-34-4656
 FEATURES
 source
 location/Qualifiers
 1. .42
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630";
 ORIGIN
 Query Match 3.0%; Score 20.2; DB 6; Length 42;
 Best Local Similarity 68.3%; Pred. No. 9e+06;
 Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 PAT 02-AUG-2002
 LOCUS BD013091
 DEFINITION Method for producing male-sterile plant.
 ACCESSION BD013091
 VERSION BD013091.1 GI:22093380
 KEYWORDS WO 0124616-A/2.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences
 REFERENCES
 AUTHORS Hamada,K. and Nakakido,F.
 TITLE Method for producing male-sterile plant
 JOURNAL Patent: WO 0124616-A 2 12-APR-2001;
 COMMENT JAPAN TOBACCO INC, KAZUYUKI HAMADA, FUMIO NAKAKIDO
 OS Artificial sequence
 PN WO 0124616-A/2
 PD 12-APR-2001
 PF 12-SEP-2000 WC 2000JPD06227
 PR 30-SEP-1999 JP 99P 279307
 PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
 PC AC1H570/C, C12N15/11, C12N15/63, C12N15/82
 CC Primer 172del-R
 FEATURES
 source
 location/Qualifiers
 1. .42
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630";
 ORIGIN
 Query Match 3.0%; Score 20.2; DB 6; Length 42;
 Best Local Similarity 68.3%; Pred. No. 9e+06;
 Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 PAT 03-JUL-2001
 LOCUS AX173088/C
 DEFINITION Sequence 67 from Patent WO0142294.
 ACCESSION AX173088
 VERSION AX173088.1 GI:14597988
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences
 REFERENCES
 AUTHORS Lu,P., Garman,J.D. and Candia,A.F.
 TITLE Clasp-4 transmembrane protein
 JOURNAL Patent: WO 0142294-A 67 14-JUN-2001;
 Arbor Vita Corporation (US)
 FEATURES
 source
 1. .50

ORIGIN /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:3230"
 /note="Exon 11 ('GR2005')"

RESULT 12
 BD247107 LOCUS BD247107 45 bp DNA linear PAT 17-JUL-2003
 DEFINITION Improved transformation efficiency in phage presentation by modification of coat proteins.
 ACCESSION BD247107
 VERSION BD247107_1 GI:33056877
 KEYWORDS JP 2002522029-A/169,
 synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 45)
 AUTHORS Sidihi,S., Weiss,G.A. and Wells,J.A.
 TITLE Improved transformation efficiency in phage presentation by modification of coat proteins.
 JOURNAL Patent: JP 2002522029-A 169 23-JUL-2002;
 COMMENT' OS Artificial Sequence
 PN JP 2002522029-A/169
 PD 23-JUL-2002
 PP 22-JUL-1999 JP 2000056299
 PR 27-JUL-1998 US 60/04291,08-OCT-1998 US 60/10314 PR
 10-MAY-1999 US 60/13296,19-MAY-1999 US 60/134870 PR
 SACHDEV S SIDHI, GREGORY A WEISS, JAMES A WELLS PC
 C12N15/09, C07K14/01, C07K14/52, C07K16/18, C07K19/00, PC
 C12N1/15,
 PC C12N1/19 C12N1/21 C12N5/10 C12N7/00, C12N15/02, C12P21/02//
 (C12P21/02, C1R1:92), C12N15/00, C12N5/00 CC sequence
 source: synthetic
 FH Key
 FT Source 1..45 Location/Qualifiers
 FT Source /organism='Artificial Sequence'.
 FEATURES Location/Qualifiers
 SOURCE 1..45
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:3230"
 ORIGIN

ORIGIN /organism="unassigned DNA"
 /mol_type="unassigned DNA"

RESULT 13
 I20781 LOCUS I20781 45 bp DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 5 from patent US 5516653.
 ACCESSION I20781
 VERSION I20781_1 GI:1601136
 KEYWORDS Unknown
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 45)
 AUTHORS Bard,J.A., Branchek,T. and Weinshank,R.L.
 TITLE DNA encoding a human neuropeptide Y peptide YY/bancreatic polypeptide receptor (Y4) and uses thereof
 JOURNAL Patent: US 5976814 A 5 02-NOV-1999;
 FEATURES Location/Qualifiers
 SOURCE 1..45
 /organism="unassigned DNA"
 /mol_type="unassigned DNA"
 ORIGIN

Query Match 3.0%; Score 20; DB 6; Length 50;
 Best Local Similarity 72.2%; Pred. No. 9.5e+06;
 Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 510 GETCCCTGAGCGAGGGTCCGTATCAGCTGAAGC 545
 Db 44 GCTCCCGCAGCTGATGTTGTCAGCCGCATC 9

RESULT 10
 AR075912/c LOCUS AR075912/c 45 bp DNA linear PAT 30-AUG-2000
 DEFINITION Sequence 5 from patent US 5958709.
 ACCESSION AR075912
 VERSION AR075912.1 GI:10002658
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)
 AUTHORS Bard,J.A., Walker,M.W., Branchek,T. and Weinshank,R.L.
 TITLE Processes for identifying compounds that bind to the human Y4 receptor
 JOURNAL Patent: US 5958709-A 5 28-SEP-1999;
 FEATURES Location/Qualifiers
 SOURCE 1..45
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 2.9%; Score 19.8; DB 6; Length 45;
 Best Local Similarity 69.2%; Pred. No. 1.1e+07;
 Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 131 GRAGGGGACCTTCAAGAAGTTGCTGAAGTTGCTGTC 169
 Db 44 GAGGGTTACGATCAGATGTTGGCATTCCTCATC 6

RESULT 11
 AR083198/c LOCUS AR083198 45 bp DNA linear PAT 01-SEP-2000
 DEFINITION Sequence 5 from patent US 5976814.
 ACCESSION AR083198
 VERSION AR083198.1 GI:10009988
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 45)
 AUTHORS Bard,J.A., Walker,M.W., Branchek,T. and Weinshank,R.L.
 TITLE DNA encoding a human neuropeptide Y peptide YY/bancreatic polypeptide receptor (Y4) and uses thereof
 JOURNAL Patent: US 5976814 A 5 02-NOV-1999;
 FEATURES Location/Qualifiers
 SOURCE 1..45
 /organism="unassigned DNA"
 /mol_type="unassigned DNA"

Query Match 2.9%; Score 19.8; DB 6; Length 45;
 Best Local Similarity 69.2%; Pred. No. 1.1e+07;
 Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 131 GACAGGACACGTTCAAGAAGTTGCTGAAGTTGCTGTC 169
 Db 44 GAGGGTTACGATCAGATGTTGGCATTCCTCATC 6

Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

PI MARIA GRACIELA CASTRO, STEPHEN CHARLES EMERY, PEDRO RICARDO PI
LOWENSEIN
PC C12N15/09, A61K31/198, A61K31/222, A61K35/76, A61K38/00, A61K38/44,
PC A61K38/46,
PC A61K48/00, A61P35/00, A61P43/00, C12N15/00, A61K37/54, A61K37/02,
PC A61K37/50
PC A61K37/50
Description of Artificial Sequence: Primer
CC
Key FH
Description of Artificial Sequence: Primer
Location/Qualifiers
FH
Key FT
Source FT
/organism='Artificial Sequence' 1..48
Location/Qualifiers
1..48
/organism='synthetic construct'
/mol type="genomic DNA"
/db_xref="taxon:32630"

RESULT 14

LOCUS BD237452 cDNA linear PAT 17-JUL-2003

DEFINITION Single nucleotide polymorphism of human pyruvate dehydrogenase kinase isoenzyme 2 (PDK2).

ACCESSION BD237452

VERSION BD7455.1 GI:33047722

KEYWORDS 200533135-A/8

SOURCE Synthetic construct

ORGANISM Synthetic construct

ARTIFICIAL SEQUENCES 1 (bases 1 to 48)

REFERENCE Anand,R., Morten,J.E.N. and Smith,J.C.

AUTHORS Morten,J.E.N. and Smith,J.C.

TITLE Single nucleotide polymorphism of human pyruvate dehydrogenase kinase isoenzyme 2 (PDK2)

JOURNAL ASTRAZENECA AB

PATENT JP 2002533135-A 8 08-OCT-2002;

COMMENT OS Artificial Sequence
PN JP 2012533135-A/8
DD 08-OCT-2002
BP 17-DEC-1999 JP 2000591219
ER 23-DEC-1999 GB 9828255, 9
EI RAKESH ANAND,JOHN EDWARD NORRIS MORTEN,JOHN CRAIG SMITH PC
C12N15/09, A61K31/711,A61K48/00, A61P3/04, A61P3/10, A61P7/00, PC
C12Q1/68
EC C12N15/00
CC Description of Artificial Sequence: Primer
FH Key
FT Source FT
/organism='Artificial Sequence' 1..48
/organism='synthetic construct'
/mol type="genomic DNA"
/db_xref="taxon:32630"

FEATURES source
ORIGIN

Query Match 2.9%; Score 19.8; DB 6; Length 48;
Best Local Similarity 63.8%; Pred. No. 1e+07; Indels 0; Gaps 0;

Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

PI MARIA GRACIELA CASTRO, STEPHEN CHARLES EMERY, PEDRO RICARDO PI
LOWENSEIN
PC C12N15/09, A61K31/198, A61K31/222, A61K35/76, A61K38/00, A61K38/44,
PC A61K38/46,
PC A61K48/00, A61P35/00, A61P43/00, C12N15/00, A61K37/54, A61K37/02,
PC A61K37/50
PC A61K37/50
Description of Artificial Sequence: Primer
CC
Key FH
Description of Artificial Sequence: Primer
Location/Qualifiers
FH
Key FT
Source FT
/organism='Artificial Sequence' 1..48
Location/Qualifiers
1..48
/organism='synthetic construct'
/mol type="genomic DNA"
/db_xref="taxon:32630"

RESULT 15

LOCUS BD270516 cDNA linear PAT 17-JUL-2003

DEFINITION Method.

ACCESSION BD270516

VERSION BD270516.1 GI:33080284
JP 2002542830-A/8.

KEYWORDS Synthetic construct

ORGANISM Synthetic construct

ARTIFICIAL SEQUENCES 1 (bases 1 to 48)

REFERENCE Authors Castro,M.G., Emery,S.C. and Lowenstein,P.R.
Title Method
Journal ASTRAZENECA AB THE VICTORIA UNIVERSITY OF MANCHESTER
Comment OS Artificial Sequence
PN JP 2002542830-A/8
PD 17-DEC-2002
PF 28-APR-2000 JP 2000615774
PR 01-MAY-1999 GB 9910077.8

RESULT 2
 US-09-993-346-463/C
 ; Sequence 463, Application US/09993346
 GENERAL INFORMATION:
 APPLICANT: Edwards, Cynthia A.
 Cantor, Charles R.
 Andrews, Beth M.
 Turin, Lisa M.
 TITLE OF INVENTION: Sequence-Directed DNA Binding Molecules, Compositions and Methods

NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genelabs Technologies, Inc.
 STREET: 505 Penobscot Drive
 CITY: Redwood City
 STATE: CA
 COUNTRY: USA
 ZIP: 94063

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/993-346
 FILING DATE: 13-Nov. US20030124530A1-2001

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/354,947
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/171,389
 FILING DATE: 20-DEC-1993
 APPLICATION NUMBER: US 08/123,936
 FILING DATE: 17-SEP-1993
 APPLICATION NUMBER: US 07/996,783
 FILING DATE: 23-DEC-1992
 APPLICATION NUMBER: US 07/723,618
 FILING DATE: 27-JUN-1991
 APPLICATION NUMBER: US 08/081,970
 FILING DATE: 22-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Brady, John F.
 REGISTRATION NUMBER: 39,118
 REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 324-0880
 TELEFAX: (650) 324-0860
 INFORMATION FOR SEQ ID NO: 463:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 50 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Human insulin-like growth factor II
 Gene
 SEQUENCE DESCRIPTION: SEQ ID NO: 463:

us-09-993-346-463

Query Match Score 20; DB 10; Length 50;
 Best Local Similarity 65.9%; Pred. No. 2.6e-04;
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 259 GCGGGCACACACACCCCTGCTTCAAGCAGGTCTCCGGCTGCC 302
 Db 49 GCGGGCGCCACGCCGGCTTATGTCGCCAGGCC 6

RESULT 3
 US-10-131-827-677

; Sequence 677, Application US/10131827
 ; Publication No. US20040009479A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Whiblemuth, Jay
 ; APPLICANT: Fry, Kirk
 ; APPLICANT: Woodward, Robert
 ; APPLICANT: Ly, Ngoc
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE DISEASES
 ; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
 ; FILE REFERENCE: 506612000120
 ; CURRENT APPLICATION NUMBER: US/10/131-827
 ; CURRENT FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: US 10/006,290
 ; PRIOR FILING DATE: 2001-10-22
 ; PRIOR APPLICATION NUMBER: US 60/296,764
 ; PRIOR FILING DATE: 2001-06-08
 ; NUMBER OF SEQ ID NOS: 9090
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 677
 ; LENGTH: 50
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-131-827-677

Query Match Score 20; DB 15; Length 50;
 Best Local Similarity 82.1%; Pred. No. 2.6e+04;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 172 GCCCTGATGGAAAGACTGAGAGAG 199
 Db 16 GCGGGATGGAAAGACAGAGAGAG 43

RESULT 4
 US-10-319-315-56
 ; Sequence 56, Application US/10319315
 ; Publication No. US2003019774A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol Myers Squibb Company
 ; TITLE OF INVENTION: NOVEL HUMAN NEUROTRANSMITTER TRANSPORTER
 ; FILE REFERENCE: D0205 NP
 ; CURRENT APPLICATION NUMBER: US/10/319,315
 ; CURRENT FILING DATE: 2002-12-13
 ; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 56
 ; LENGTH: 42
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-319-315-56

Query Match Score 20; DB 15; Length 42;
 Best Local Similarity 69.2%; Pred. No. 2.6e+04;
 Matches 27; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 23 CTCCATACTGACCATCCCCGTGACAGTGCAGTGGCC 61
 Db 3 CCCAACGTTGACCATGCCAGAACAGCAAAGTGCACC 41

RESULT 5
 US-10-011-931-8/C
 ; Sequence 8, Application US/10011931
 ; Publication No. US2003026806A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Witte, Alison
 ; APPLICANT: Varnum, Brian C.
 ; APPLICANT: Qian, Zueming
 ; APPLICANT: Vezina, Chris
 ; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BI
 ; FILE REFERENCE: A-731
 ; CURRENT APPLICATION NUMBER: US/10/011,931

CURRENT FILING DATE: 2002-04-01
 PRIORITY APPLICATION NUMBER: US 60/244,118
 PRIOR FILING DATE: 2000-10-27
 NUMBER OF SEQ ID NOS: 78
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 8
 LENGTH: 50
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: KAPPA CHAIN CHIMERA
 US-10-011-931-8

Query Match 2.9%; Score 19 6; DB 14; Length 50;
 Best Local Similarity 73.5%; Pred. No. 3.5e+04;
 Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 331 GAAGAGCTCCAGGAACCTGCATTCTCAGGATC 364
 Db 50 GAACCCAGCAGGAACCAAGTGTTCAGATC 17

RESULT 6
 US-10-131-827-309/c
 Sequence 339, Application US/10131827
 GENERAL INFORMATION:
 APPLICANT: Wohlgemuth, Jay
 FRY, Kirk
 APPLICANT: Woodward, Robert
 APPLICANT: Ly, Ngoc
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE DISEASES
 FILE REFERENCE: 506112000120
 CURRENT FILING DATE: 2002-09-06
 PRIOR APPLICATION NUMBER: US 10/006, 290
 PRIOR FILING DATE: 2001-10-22
 PRIOR APPLICATION NUMBER: US 60/296, 764
 PRIOR FILING DATE: 2001-06-08
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 309
 LENGTH: 50
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-10-131-827-309

Query Match 2.9%; Score 19.4; DB 15; Length 50;
 Best Local Similarity 64.4%; Pred. No. 4e+04;
 Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 195 AGAGCTTGGAGAACTTGGTCCAGGCCAACCTGTACAGAGA 239
 Db 45 AGAGAAAGGGGATACTTGGTCAACGCCAGCAAAAGATA 1

RESULT 7
 US-09-817-464-19/c
 Sequence 19, Application US/09817464
 PATENT NO. US200212763BA1
 GENERAL INFORMATION:
 APPLICANT: Flor, Peter J.
 APPLICANT: Kuhn, Ranier
 APPLICANT: Lindauer, Kristen
 APPLICANT: Puttner, Irene
 APPLICANT: Knopfel, Thomas
 TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4, HMR6, HMR7) and Related DNA Compounds
 FILE REFERENCE: 4-19679/A/PCT
 CURRENT APPLICATION NUMBER: US/10/331,289
 CURRENT FILING DATE: 2002-12-10
 PRIOR APPLICATION NUMBER: US/08/617,785
 PRIOR FILING DATE: 1996-02-19
 PRIOR APPLICATION NUMBER: PCT/EP94/02991
 PRIOR FILING DATE: 1994-03-07
 PRIOR APPLICATION NUMBER: EP 9416553.7
 PRIOR FILING DATE: 1994-04-19
 PRIOR APPLICATION NUMBER: EP 93810663.0
 PRIOR FILING DATE: 1993-09-20
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 19
 LENGTH: 44
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:
 US-10-331-289-19

Query Match 2.9%; Score 19 2; DB 14; Length 44;
 Best Local Similarity 67.5%; Pred. No. 4.5e+04;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 266 CACACACCCTGCTCAGCAGGCTCTCGCTGCCCCCTGCG 305
 Db 42 CCCGCTCTAGCCCTAGCAGGCCCTCGGccGcGcGcGcGc 3

RESULT 9
 US-10-349-143-2676
 Sequence 26, Application US/10349143
 Publication No. US2004005584A1
 GENERAL INFORMATION:

APPLICANT: Cohen, Daniel
 APPLICANT: Blumenfeld, Marta
 APPLICANT: Chumakov, Ilya
 TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
 CURRENT APPLICATION NUMBER: US/10/349,143
 CURRENT FILING DATE: 2003-01-21
 PRIOR APPLICATION NUMBER: US/09/422,978
 PRIOR FILING DATE: 1999-10-20
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
 NUMBER OF SEQ ID NOS: 11796
 SEQ ID NO: 2676
 LENGTH: 47
 TYPE: DNA
 ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: allele
 LOCATION: 24
 OTHER INFORMATION: 99-13864-64 : polymorphic base G or T
 US-10-349-143-2676

Query Match 2.3%; Score 19.2; DB 15; Length 47;
 Best Local Similarity 70.6%; Pred. No. 4.6e-04;
 Matches 24; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
 SEQ 272 CCCTGCTCAGGAGGTCTCCGGCTCCCCCTGC 305
 Db 10 CCCTCCCTCCACAGKCTGCTCCCTGC 43

RESULT 10
 US-10-131-827-1287
 Sequence 1287, Application US/10131827
 Publication No. US2004009479A1
 GENERAL INFORMATION:
 APPLICANT: Wohlgemuth, Jay
 APPLICANT: Fry, Kirk
 APPLICANT: Woodward, Robert
 APPLICANT: Ly, Ngoc
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE DISEASES
 FILE REFERENCE: 506612000120
 CURRENT APPLICATION NUMBER: US/10/131,827
 CURRENT FILING DATE: 2002-09-06
 PRIOR APPLICATION NUMBER: US 10/006,290
 PRIOR FILING DATE: 2001-10-22
 PRIOR APPLICATION NUMBER: US 60/296,764
 PRIOR FILING DATE: 2001-06-08
 NUMBER OF SEQ ID NOS: 9090
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1287
 LENGTH: 50
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-131-827-1287

Query Match 2.9%; Score 19.2; DB 15; Length 50;
 Best Local Similarity 67.5%; Pred. No. 4.7e-04;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 67 AGTTTCTGGGTCCAGCCCTCTCCAGAACTGACCGCG 106
 Db 11 AGTCCCTGTGTCAGCCATCCAGGGTTTGCTG 50

RESULT 11
 US-10-131-827-1362/C
 Sequence 1362, Application US/10131827

; Publication No. US2004009479A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlgemuth, Jay
 ; APPLICANT: Fry, Kirk
 ; APPLICANT: Woodward, Robert
 ; APPLICANT: Ly, Ngoc
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE DISEASES
 ; FILE REFERENCE: 506612000120
 ; CURRENT APPLICATION NUMBER: US/10/131,827
 ; CURRENT FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: US 10/006,290
 ; PRIOR FILING DATE: 2001-10-22
 ; PRIOR APPLICATION NUMBER: US 60/296,764
 ; PRIOR FILING DATE: 2001-06-08
 ; NUMBER OF SEQ ID NOS: 9090
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 1362
 ; LENGTH: 50
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-131-827-1362

Query Match 2.9%; Score 19.2; DB 15; Length 50;
 Best Local Similarity 67.5%; Pred. No. 4.7e-04;
 Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 178 CATGGAAAGACTGCGAGAGCTGGGGCAACCTGGTG 217
 Db 42 CAGGTGGRAGATGCAAAAAGCTTTAGAACATAGATG 3

RESULT 12
 US-09-978-917A-23
 ; Sequence 23, Application US/09978917A
 ; Publication No. US2003002729A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maxygen Apps Maxygen Holdings
 ; TITLE OF INVENTION: Protein C or activated protein C-like molecules
 ; FILE REFERENCE: 0219us10 - Protein C
 ; CURRENT APPLICATION NUMBER: US/09/978,917A
 ; CURRENT FILING DATE: 2001-10-17
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 23
 ; LENGTH: 50
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial sequence: Primer
 ; US-09-978-917A-23

Query Match 2.8%; Score 18.8; DB 10; Length 50;
 Best Local Similarity 63.0%; Pred. No. 6.3e-04;
 Matches 29; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 465 CCGTGGGGGGGATCTAACCGGGCATCTGAGTCGCCGC 510
 Db 1 CCCCTGCAGTGGTCTGCTGACTAACCAAAGAGCTGGCCGC 46

RESULT 13
 US-10-138-195-31
 ; Sequence 31, Application US/10138195
 ; Publication No. US20030207349A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morre, D. James
 ; APPLICANT: Morre, Dorothy J.
 ; APPLICANT: Chueh, Pin Ju
 ; TITLE OF INVENTION: Sequences Encoding Human Neoplastic Marker
 ; FILE REFERENCE: 85.99
 ; CURRENT APPLICATION NUMBER: US/10/138,195
 ; CURRENT FILING DATE: 2002-05-01

PRIOR APPLICATION NUMBER: US 60/162,644
 PRIOR FILING DATE: 1999-11-01
 PRIOR APPLICATION NUMBER: PCT US00/30190
 PRIOR FILING DATE: 2000-11-01
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 31
 LENGTH: 38
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
 OTHER INFORMATION: useful as primer, for example
 US-10-138-195-31

Query Match 2.8%; Score 18.6; DB 15; Length 38;
 Best Local Similarity 72.7%; Pred. No. 6.7e+04; Indels 0; Gaps 0;
 Matches 24; Conservative 9; Mismatches 9;

Qy 358 CAGGATCTAATTGGAGATTGGCCAGTGTGGCA 390
 Db 1 CAGGAATGACTGGATTCAGGCTGGCCAGCGTGGAA 33

RESULT 14
 US-10-138-195-32/C
 Sequence 32, Application US/10138195
 Publication No. US2003020340A1

GENERAL INFORMATION:
 APPLICANT: More, D. James
 APPLICANT: More, Dorothy J.
 APPLICANT: Chuah, Bin-Ju
 TITLE OF INVENTION: Sequences Encoding Human Neoplastic Marker
 FILE REFERENCE: 85-39

CURRENT APPLICATION NUMBER: US/10138-195
 CURRENT FILING DATE: 2002-05-01
 PRIOR APPLICATION NUMBER: US 60/162,644
 PRIOR FILING DATE: 1999-11-01
 PRIOR APPLICATION NUMBER: PCT US00/30190
 PRIOR FILING DATE: 2000-11-01
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 32
 LENGTH: 38
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
 OTHER INFORMATION: useful as primer, for example
 US-10-138-195-32

Query Match 2.8%; Score 18.6; DB 15; Length 38;
 Best Local Similarity 72.7%; Pred. No. 6.7e+04; Indels 0; Gaps 0;
 Matches 24; Conservative 9; Mismatches 9;

Qy 358 CAGGATCTAATTGGAGATTGGCCAGTGTGGCA 390
 Db 38 CAGGAAATGACTGGATTCAGGCTGGCCAGCTGGAA 6

RESULT 15
 US-10-176-255-15
 Sequence 15, Application US/10176255
 Publication No. US20030153004A1

GENERAL INFORMATION:
 APPLICANT: Behan, Dominic P.
 APPLICANT: Chalmers, Derek T.
 APPLICANT: Liaw, Chen W.
 APPLICANT: Russo, Joseph F.
 APPLICANT: Thomsen, William J.
 TITLE OF INVENTION: No. US20030153004A1-Endogenous Constitutively Activated Human Se
 FILE REFERENCE: AREN-0328

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Gencore version 5.1.6
OM nucleic - nucleic search, using sw model.

Run on: February 29, 2004, 10:05:31 ; Search time 2724.97 Seconds
(without alignments)
10688.739 Million cell updates/sec

Title: US-09-904-568-1_COPY_132_803

Perfect score: 672

Sequence: 1 atgttgtttttggggctgc.....gttagcgccaaactgcaggac 672

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
 1: gb_ba:
 2: gb_htg:
 3: gb_in:
 4: gb_om:
 5: gb_nv:
 6: gb_dat:
 7: gb_ph:
 8: gb_dl:
 9: gb_pr:
 10: gb_ro:
 11: gb_sts:
 12: gb_sy:
 13: gb_un:
 14: gb_vl:
 15: em_da:
 16: em_fun:
 17: em_hum:
 18: em_in:
 19: em_mu:
 20: em_om:
 21: em_or:
 22: em_ov:
 23: em_pat:
 24: em_ph:
 25: em_pl:
 26: em_ro:
 27: em_sts:
 28: em_un:
 29: em_vl:
 30: em_htg_hum:
 31: em_htg_inv:
 32: em_htg_other:
 33: em_htg_mus:
 34: em_htg_pln:
 35: em_htg_rnd:
 36: em_htg_mam:
 37: em_htg_vrt:
 38: em_sy:
 39: em_htgo_hum:
 40: em_htgo_mus:
 41: em_htgo_other:
 Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
c 1	21.8	3.2	4.9	6	AX404880	Sequence AX404880 Cell usef
c 2	21.4	3.2	5.0	6	BD17394	Sequence BD17394 Cell usef
c 3	21.2	3.2	4.7	6	AR284756	Sequence AR284756
c 4	21	3.1	4.0	6	E14011	Probe. 7/19
c 5	20.8	3.1	4.2	6	AX710949	Sequence AX710949
c 6	20.8	3.1	4.2	6	BD001090	Method an
c 7	20.8	3.1	4.2	6	BD001519	Method an
c 8	20.6	3.1	4.1	6	AX511286	Sequence AX511286
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c 11	20.2	3.0	3.5	6	E22807	Method For
c 12	20.2	3.0	3.5	6	AR203329	Sequence AR203329
c 13	20	3.0	5.0	6	AR032851	Sequence AR032851
c 14	20	3.0	5.0	6	I29591	Sequence I29591
c 15	20	3.0	5.0	6	I91265	Sequence I91265
c 16	20	3.0	5.0	6	AR209515	Sequence AR209515
c 17	20	3.0	5.0	6	AJ00712	Abaidops
c 18	19.8	2.9	4.6	6	AR157914	Sequence AR157914
c 19	19.4	2.9	5.0	6	AX199530	Sequence AX199530
c 20	19.2	2.9	5.2	6	BD61703	Antigenic
c 21	19.2	2.9	4.4	6	AR149584	Sequence AR149584
c 22	19.2	2.9	4.7	6	AR20941	Sequence AR20941
c 23	19	2.8	2.7	6	AR089960	Sequence AR089960
c 24	19	2.8	2.7	6	AR19695	Sequence AR19695
c 25	19	2.8	2.7	6	AR259149	Sequence AR259149
c 26	18.8	2.8	4.2	6	AX080016	Sequence AX080016
c 27	18.8	2.8	4.3	6	AX466471	Sequence AX466471
c 28	18.8	2.8	4.8	6	S77040	T-cell rece
c 29	18.8	2.8	5.0	6	BD225137	Polymer
c 30	18.6	2.8	4.3	6	AR107092	Sequence AR107092
c 31	18.6	2.8	4.3	6	AR111855	Sequence AR111855
c 32	18.6	2.8	4.3	6	AR118372	Sequence AR118372
c 33	18.6	2.8	4.3	6	AR302214	Sequence AR302214
c 34	18.6	2.8	4.3	6	AX813374	Sequence AX813374
c 35	18.6	2.8	4.3	6	BD132482	Binding m
c 36	18.6	2.8	4.7	6	AX236856	Sequence AX236856
c 37	18.4	2.7	3.1	6	AX286510	Sequence AX286510
c 38	18.4	2.7	3.7	6	AR012326	Sequence AR012326
c 39	18.4	2.7	3.7	6	AR012348	Sequence AR012348
c 40	18.4	2.7	3.7	6	BD059047	Sequence BD059047
c 41	18.4	2.7	3.9	6	E49257	Omega 3 fat
c 42	18.4	2.7	4.0	6	AX538550	Sequence AX538550
c 43	18.4	2.7	4.7	6	I77232	Sequence 22
c 44	18.4	2.7	4.8	6	AX582839	Sequence AX582839
c 45	18.4	2.7	5.0	6	AR252548	Sequence AR252548

ALIGNMENTS

RESULT 1
 AX404880/C
 LOCUS Sequence 13 from Patent WO0222833.
 DEFINITION AX404880
 ACCESSION AX404880
 VERSION GI:21438112
 KEYWORDS SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 1 Pfizermaier, K., Wuest, T., Moosmayer, D., Grell, M. and Scheurich, P.
 Fusion Protein from antibody cytokine-cytokine inhibitor
 (selectoKine) for use as target-specific prodrug
 Patent: WO 0222833-A 13 21-MAR-2002;
 JOURNAL

Universitaet Stuttgart (DE) ; Pfizenmaier, Klaus (DE)
Location/Qualifiers
1. -49
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref=taxon:32610"
/note="Primer 4 fuer die Amplifikation eines humanen
TNTF-fragmentes."
FEATURES
source

AUTHORS Blumenfeld, M., Chumakov, I., Bougeieret, L. and Cohen, A.
 TITLE Biallelic markers related to genes involved in drug metabolism
 JOURNAL Patent : US 6528260-A 08 04-MAR-2003;
 FEATURES Location/Qualifiers
 source 1. .47
 /organism="unknown"
 /mol_type="genomic DNA"

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						Gaps	0;
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Db	46	TGGATCATGCCCTGCGGAAATCGAGCTGGCTAG	6				
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LOCUS		Cell useful for evaluation of sex hormone receptor.					
DEFINITION							
ACCESSION	BD174394						
VERSION	BD174394.1	GI:29120078					
KEYWORDS							
SOURCE							
ORGANISM							
COMMENT							
REFERENCE	1 (bases 1 to 50)						
AUTHORS	Nakao,T., Matsue,K. and Takebayashi,N.						
TITLE	Cell useful for evaluation of action of sex hormone receptor						
JOURNAL	Patent: JP 2002247986-A 27 05-SEP-2002;						
MITSUJI CHEMICALS INC							
OS	Artificial Sequence						
PN	JP 2002247986-A/27						
PD	03-SEP-2002						
PF	23-FEB-2001	JP 2001048875					
PI	TOSHIFUMI NAKAO, KAORI MATSUE, NOZOMI TAKEBAYASHI	PC					
C12N1/02,C12N5/10,C12Q1/66,(C12Q1/66,C12R1:91), C12N15/00, C12N5/00,	PC						
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Key							
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FT	Location/Qualifiers						
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Best Local Similarity	66.0%;	Pred. No. 1e+06;					
Matches	31;	Conservative	0;	Mismatches	16;	Indels	0;
						Gaps	0;
Qy	136	AGGACCTTCAAGAAGTGTGAACACTGAGCTGAGCTGG 182					
Db	4	AGCTTCCTGGCAAGCCTGTTGACGCTTGTGGCTGGCAGGG 50					
RESULT 3	RB284756/C	AR284756	47 bp	DNA	linear	PAT 10-APR-2003	
LOCUS		Sequence 808 from patent US 6528260.					
DEFINITION							
ACCESSION	AR284756						
VERSION	AR284756.1	GI:29721660					
KEYWORDS							
ORGANISM	Unknown.						
COMMENT	Unknown.						
REFERENCE	1 (bases 1 to 47)						
RESULT 4	E14011	E14011	40 bp	DNA	linear	PAT 28-JUL-1999	
LOCUS							
DEFINITION	Probe						
ACCESSION	E14011						
VERSION	E14011.1	GI:5708694					
KEYWORDS							
SOURCE							
ORGANISM	unidentified						
COMMENT	unclassified.						
REFERENCE	1 (bases 1 to 40)						
AUTHORS	Shimada, K. and Namatame, Y.						
TITLE	IMMOBILIZATION OF GENE						
JOURNAL	PATENT: JP 1997257798-A.1 03-OCT-1997;						
SUMITOMO METAL IND LTD							
OS	None						
COMMENT	OS Artificial sequences.						
PN	JP 1997257798-A/1						
PD	03-OCT-1997						
PP	PP						
PI	SHIMADA KAZUNORI, NAMATAME YASUO	PC					
CN	PC 01N33/566 C12N15/09 C12Q1/68;	CC					
CC	strandedness: Single;	CC					
topology: Linear;	CC						
hypothetical: No;	CC						
anti-sense: No;	CC						
Key	FH						
COMMENT	Location/Qualifiers						
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1..40	/organism='Artificial sequences'.						
FEATURES	source						
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Best Local Similarity	73.0%;	Pred. No. 1.3e+06;					
Matches	27;	Conservative	0;	Mismatches	10;	Indels	0;
						Gaps	0;
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Db	4	GTCTCACTCTATGCCTTCAGTAGCTCTGGAA 40					
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LOCUS							
DEFINITION							
ACCESSION	Sequence 249 from Patent EP1288296.						
VERSION	AX710949						
KEYWORDS							
SOURCE	HUMAN HERPESVIRUS 5						
ORGANISM	Human herpesvirus 5						

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.

1 REFERENCE
AUTHORS Draper K.G., McSwigen,J.A., Holecek,J.J., Dudycz,I.W.,
Macejek,D.G. and Mamone,A.J.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288286-A 249 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source
1. .42
/organism="Human herpesvirus 5"
(mol_type="unassigned RNA"
/db_xref="taxon:10359"

ORIGIN

Query Match 3.1%; Score 20.8; DB 6; Length 42;
Best Local Similarity 70.0%; Pred. No. 1.5e+06;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 201 TGTGAGCAACTTGGGCCAGGCCAACCTGTCAAGAGG 240
Db 2 TGTGATGACCTACGGCATGCCAGAGTCGATGAG 41

RESULT 7

BD001519 42 bp RNA linear PAT 31-JAN-2002
LOCUS BD001519
DEFINITION Method and reagent for inhibiting viral replication.
VERSION BD001519_1 GI:18626078
KEYWORDS JP 2000342286-A/250.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 42)
AUTHORS Draper,K.G., Dadykitz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 250 12-DEC-2000;

COMMENT

OS Artificial Sequence
PN JP 2000342286-A/250
PF 01-DEC-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882714 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882886 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882891 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/882923 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/883849 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884074 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
26-AUG-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
15-OCT-1992 US 07/936086,18-SEP-1992 US 07/943359 PR
07-DEC-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
KENNETH G DRAPER, LEC W DADYKIZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLSEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, A61K39/125, A61K39/13,
PC A61K39/135,
PC A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K48/00,
PC A61P1/16,
PC A61P31/14, A61P31/16, A61P31/18, A61P35/02, A61P68/00,
(C12N5/09, C12R1:93), C12N5/00, C12R1:93, (C12N5/00, C12R1:93)

COMMENT

OS Artificial Sequence
PN JP 2000342286-A/250
PF 12-DEC-2000 JP 2000132616
PR 01-MAY-1992 US 07/882713,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
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14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/933738,26-AUG-1992 US 07/935854 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PR
KENNETH G DRAPER, LEC W DADYKIZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLSEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22 // (C12N5/10, C12R1:91), PC
C12N5/00, (C12N5/00, C12R1:91)

COMMENT

OS Artificial Sequence
PN JP 2000342286-A/250
PF 12-DEC-2000 JP 2000132616
PR 01-MAY-1992 US 07/882713,14-MAY-1992 US 07/882712 PR
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14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/933738,26-AUG-1992 US 07/935854 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PR
KENNETH G DRAPER, LEC W DADYKIZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLSEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22 // (C12N5/10, C12R1:91), PC
C12N5/00, (C12N5/00, C12R1:91)

COMMENT

OS Artificial Sequence
PN JP 2000342286-A/250
PF 12-DEC-2000 JP 2000132616
PR 01-MAY-1992 US 07/882713,14-MAY-1992 US 07/882712 PR
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14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/933738,26-AUG-1992 US 07/935854 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PR
KENNETH G DRAPER, LEC W DADYKIZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLSEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22 // (C12N5/10, C12R1:91), PC
C12N5/00, (C12N5/00, C12R1:91)

ORIGIN

Query Match 3.1%; Score 20.8; DB 6; Length 42;
Best Local Similarity 70.0%; Pred. No. 1.5e+06;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 201 TGTGAGCAACTTGGGCCAGGCCAACCTGTCAAGAGG 240
Db 2 TGTGATGACCTACGGCATGCCAGAGTCGATGAG 41

RESULT 7

BD001519 42 bp RNA linear PAT 31-JAN-2002
LOCUS BD001519
DEFINITION Method and reagent for inhibiting viral replication.
VERSION BD001519_1 GI:18626078
KEYWORDS JP 2000342286-A/250.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 42)
AUTHORS Draper,K.G., Dadykitz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 250 12-DEC-2000;

COMMENT

OS Artificial Sequence
PN JP 2000342286-A/250
PF 01-DEC-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882714 US 07/882714 PR
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14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
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14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
26-AUG-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PR
KENNETH G DRAPER, LEC W DADYKIZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLSEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22 // (C12N5/10, C12R1:91), PC
C12N5/00, (C12N5/00, C12R1:91)

ORIGIN

Query Match 3.1%; Score 20.8; DB 6; Length 42;
Best Local Similarity 70.0%; Pred. No. 1.5e+06;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 201 TGTGAGCAACTTGGGCCAGGCCAACCTGTCAAGAGG 240
Db 2 TGTGATGACCTACGGCATGCCAGAGTCGATGAG 41

RESULT 8

AX514286 / C AX514286 41 bp DNA linear PAT 05-OCT-2002
 LOCUS Sequence 484 from Patent WO02052044.
 DEFINITION
 ACCESSION AX514286
 VERSION AX514286..1 GI:23560673
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 Nakamura, Y.; Sekine,A.; Iida,A. and Saito,S.
 AUTHORS
 TITLE Detection of genetic polymorphisms
 JOURNAL Patent: WO 02052044-A 484 04-JUL-2002;
 Riken (JP)
 FEATURES Location/Qualifiers
 source 1..41
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9605"

ORIGIN

Query Match 3.1%; Score 20.6; DB 6; Length 41;
 Best Local Similarity 70.3%; Pred. No. 1.7e+06;
 Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 20 CAGCTCCATACTGCACCATCCCGCTGACAGTCACG 56
 Db 38 CAGCCCTGTAACTGCACATCCTGCTGGGTCCTCGG 2

RESULT 9

AX520468 / C AX520468 41 bp DNA linear PAT 05-OCT-2002
 LOCUS Sequence 6666 from Patent WO02052044.
 DEFINITION
 ACCESSION AX520468
 VERSION AX520468..1 GI:23571065
 KEYWORDS
 SOURCE
 Homo sapiens (human)
 Organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 Nakamura, Y.; Sekine,A.; Iida,A. and Saito,S.
 AUTHORS
 TITLE Detection of genetic polymorphisms
 JOURNAL Patent: WO 02052044-A 6666 04-JUL-2002;
 Riken (JP)
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ORIGIN

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 Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 20 CAGCTCCATACTGCACCATCCCGCTGACAGTCACG 56
 Db 38 CAGCCCTGTAACTGCACATCCTGCTGGGTCCTCGG 2

RESULT 10

AR284587 AR284587 47 bp DNA linear PAT 10-APR-2003
 LOCUS Sequence 639 from Patent US 6528260.
 DEFINITION
 ACCESSION AR284587
 VERSION AR284587..1 GI:29721491
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE

1 (bases 1 to 47)
 AUTHORS Blumenfeld,M.; Chumakov,I.; Bougueret,L. and Cohen,A.
 TITLE Blumenfeld markers related to Genes involved in drug metabolism
 JOURNAL Patent: US 6528260-A 639 04-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..47
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ORIGIN

Query Match 3.1%; Score 20.6; DB 6; Length 47;
 Best Local Similarity 64.4%; Pred. No. 1.7e+06;
 Matches 29; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

Qy 596 AGCTGGTGTACAGTGTTAGGAGATGGCAGAAC 640
 Db 3 AGTAGGGGACACTGAACCATRGGGGCCAGGCTGCCAGAGC 47

RESULT 11

E22807 E22807 35 bp DNA linear PAT 18-JUN-2001
 LOCUS E22807 Method for screening PPAR agonist and antagonist.
 DEFINITION E22807 Method for screening PPAR agonist and antagonist.
 ACCESSION E22807
 VERSION E22807..1 GI:13024121
 KEYWORDS JP 1999053369-A/2.
 SOURCE unidentified
 ORGANISM unclassified
 REFERENCES 1 (bases 1 to 35)
 AUTHORS Junko,M. and Tomoyasu,T.
 TITLE Method for screening PPAR agonist and antagonist.
 JOURNAL TANABE SEIYAKU CO LTD
 COMMENT OS unidentified
 PN JP 199053369-A/2
 PD 02-MAR-1999
 PR 27-AUG-1997 JP 1997231084
 PI JUNKO MINAKAMI, TOMOYASU TANIGUCHI
 PC C12N15/09 C12N1/19, C12Q1/68// (C12N1/19, C12R1:645), C12N15/00 CC
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key
 FT Source 1..35
 PT Source /organism='Unidentified'.
 FEATURES Location/Qualifiers
 source 1..35
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 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 3.0%; Score 20.2; DB 6; Length 35;
 Best Local Similarity 75.8%; Pred. No. 2.2e+06;
 Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 86 CCTCCAGAAGTCACGGCGTGGCTGCTCT 118
 Db 1 CCGCTGAGAAATGTTGGCAAGTGGCTGAGTCAGGACT 33

RESULT 12

AR203329 AR203329 35 bp DNA linear PAT 20-JUN-2002
 LOCUS Sequence 2 from patent US 6363361.
 DEFINITION AR203329
 ACCESSION AR203329..1 GI:21499690
 VERSION
 KEYWORDS Unknown.

ORGANISM Unknown; Unclassified.
 REFERENCE 1 (bases 1 to 35)
 AUTHORS Taniguchi, T. and Mizukami, J.
 TITLE Method for identifying or screening agonist and antagonist to PPAR
 JOURNAL Patent : US 635361-A 2 02-APR-2002;
 FEATURES Location/Qualifiers 1..35
 source /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 3.0%; Score 20.2; DB 6; Length 35;
 Best Local Similarity 55.8%; Pred. No. 2.2e+06;
 Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 86 CCTCTCAGAAGTGAACGGCGGGTCAGTCT 118
 Db 1 CCGCTGAGAAATGTGCAAGTGGCTTCAAGACT 33

RESULT 13
 AR032851/c AR032851 50 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 463 from patent US 5869241.
 ACCESSION AR032851
 VERSION AR032851.1 GI:5948456
 KEYWORDS Unknown; Unclassified.
 SOURCE
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
 TITLE Method of determining DNA sequence preference of a DNA-binding
 molecule
 JOURNAL Patent : US 5869241-A 463 09-FEB-1999;
 FEATURES Location/Qualifiers 1..50
 source /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 3.0%; Score 20; DB 6; Length 50;
 Best Local Similarity 65.9%; Pred. No. 2.4e+06;
 Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 259 GCGGGCACACACACCCGCTCCAGGGTCTCGGGTGCCTCCC 302
 Db 49 GCGGGGCCACGGCTCTATAGTGCGCAGCGCAG 6

RESULT 14
 I29591/c I29591 50 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 463 from patent US 5578444.
 ACCESSION I29591
 VERSION I29591.1 GI:1820382
 KEYWORDS Unknown.
 SOURCE
 ORGANISM Unknown; Unclassified.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
 TITLE Sequence-directed DNA-binding molecules compositions and methods
 JOURNAL Patent : US 5578444-A 463 26-NOV-1996;
 FEATURES Location/Qualifiers 1..50
 source /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 3.0%; Score 20; DB 6; Length 50;
 Best Local Similarity 65.9%; Pred. No. 2.4e+06;

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GenCore version 5.1.6
 OM nucleic - nucleic search, using sw model
 Run on: February 29, 2004, 10:34:43 ; Search time 2031.49 Seconds
 (without alignments)
 9878.168 Million cell updates/sec

Title: US-09-904-568-1_COPY_132_803
 Perfect score: 672
 Sequence: 1 atgtctgttgggggtgc.....gttagccaaactggaggac 672

Scoring table: IDENTITY_NUC
 Gappx 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 138346

Minimum DB seq length: 0
 Maximum DB seq length: 50

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : EST:
 1: em_estba:
 2: em_esthum:
 3: em_estin:
 4: em_estmu:
 5: em_estov:
 6: em_estpl:
 7: em_estro:
 8: em_htc:
 9: gb_est1:
 10: gb_est2:
 11: gb_htc:
 12: gb_est3:
 13: gb_est4:
 14: gb_est5:
 15: em_estfun:
 16: em_estom:
 17: em_gss_hum:
 18: em_gss_inv:
 19: em_gss_pln:
 20: em_gss_vrt:
 21: em_gss_fun:
 22: em_gss_nam:
 23: em_gss_nus:
 24: em_gss_pro:
 25: em_gss_cod:
 26: em_gss_Dbhg:
 27: em_gss_vrl:
 28: gb_gssi:
 29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
 AU106355/C
 LOCUS AU106355 Sugano Homo sapiens mRNA
 DEFINITION KAT02156, mRNA sequence.
 ACCESSION AU106355
 VERSION AU106355.1 GI:13555876
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 212/0072
 PUBMED 11375929
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo,
 4-1-6, Shirakane-dai, Minatoku, Minato-ku, Tokyo 108-0039, Japan
 Email: ybsuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Matsumura, A., and Suyama, A. and

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	3.3	50	9 AU106355	AU106355
C 2	20.6	3.1	50	9 AU104945	AU104945
C 3	20.4	3.0	40	9 AA933550	AA933550 om56C06..S
C 4	20.4	3.0	49	28 AZ971265	AZ971265 2M0244N12

ALIGNMENTS

FEATURES	Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).	similar to SW:DPD2_HUMAN P49005 DNA POLYMERASE DELTA SMALL SUBUNIT 1', mRNA sequence.
source	Location/Qualifiers 1..50 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="Taxon:9606" /clone_lib="Sugano Homo sapiens cDNA library"	ACCESSION AA933650.1 GI:3089918 VERSION EST. KEYWORDS Homo sapiens (human) SOURCE Homo sapiens ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index TITLE Unpublished (1997) COMMENT Contact: Robert Strausberg, Ph.D. Email: Cgabs-remail.nih.gov Tissue Procurement: Christopher A. Moskalkuk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lemmon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bioc.lnl.gov/bbtp/image/image.html
ORIGIN	Query Match 3.3%; Score 22; DB 9; Length 50; Best Local Similarity 73.7%; Pred. No. 3e+05; Indels 0; Gaps 0; Matches 28; Conservative 0; Mismatches 10;	JOURNAL Tissue considered overall poor quality Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1. COMMENT Location/Qualifiers 1..40 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="Taxon:9606" /clone=IMAGE:1501178 /tissue_type="poole germ cell tumors" /lab_hst="IDH10B" /clone.lib=NCI CGAP GC4" /note="vector: PT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pPT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
RESULT 2	AU104945 LOCUS AU104945 Definition HRC05721, mRNA sequence.	ORIGIN Query Match Best Local Similarity 71.1%; Pred. No. 6.5e+05; Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0; COMMENT SOURCE Mus musculus (house mouse) ORGANISM Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus. REFERENCE Dunn,D., Ayagi,A., Barber,M., Beacons,T., Duval,B., Hamil,C., Islam,H., Longaire,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
FEATURES	Query Match 3.1%; Score 20.6; DB 9; Length 50; Best Local Similarity 74.3%; Pred. No. 6.6e+05; Indels 0; Gaps 0; Matches 26; Conservative 0; Mismatches 9;	RESULT 4 AZ971265/C LOCUS AZ971265 DEFINITION 2N024N12R Mouse 10kb plasmid UJGC2N library Mus musculus genomic clone UJGC2N024N12_R, genomic survey sequence.
source	/clone="HRC05721" /clone.lib="Sugano Homo sapiens cDNA library"	ACCESSION AZ971265 VERSION AZ971265.1 GI:13842492 KEYWORDS GSS. SOURCE Mus musculus (house mouse) ORGANISM Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. REFERENCE 1 (bases 1 to 49) AUTHORS Dunn,D., Ayagi,A., Barber,M., Beacons,T., Duval,B., Hamil,C., Islam,H., Longaire,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
ORIGIN	Query Match 3.1%; Score 20.6; DB 9; Length 50; Best Local Similarity 74.3%; Pred. No. 6.6e+05; Indels 0; Gaps 0; Matches 26; Conservative 0; Mismatches 9;	RESULT 3 AA933350 LOCUS AA933350.1 GI:1551178 DEFINITION om56c06.s1 NCI_CGAP_GC4 40 bp mRNA linear EST 27-APR-1998
Db	270 CACCTGTCCAGGGCTCTCGGGCTGCCCTTG 304 45 CACTCTGTCGAGGCACTCACGGCTCCCTTG 11	Db

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dundun@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0244 row: N column: 12 Seq primer: CACAGGAAACAGCTATGACC Class: Plasmid ends FEATURES source	JOURNAL MEDLINE PUBLISHED COMMENT	mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001) Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-6539, Japan Email: yasuzuki@ims.u-tokyo.ac.jp Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES source	1. 50 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="COL00924" /clone_lib="Sugano Homo sapiens cDNA library"	FEATURES source	Location/Qualifiers
ORIGIN	Query Match Best Local Similarity 3.0%; Score 20.4; DB 9; Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Qy 264 CACACAGCCCGTCAAGCAGGTCTCGGTCTGGCCC 301 Db 49 CCCACGCCAACGACTCCCGGTCTCAGCGGCC 12	ORIGIN	1. 50 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="COL00924" /clone_lib="Sugano Homo sapiens cDNA library"
RESULT 6	Query Match Best Local Similarity 3.0%; Score 20.4; DB 9; Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Qy 252 CCTGCTGGGGCACACACACCCGTCTCAGCAGCTC 289 Db 42 CCAGAGGGCACCGATGCGCTCTCCAGAGCTC 5	RESULT 6	Query Match Best Local Similarity 3.0%; Score 20.4; DB 9; Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0; Qy 252 CCTGCTGGGGCACACACACCCGTCTCAGCAGCTC 289 Db 42 CCAGAGGGCACCGATGCGCTCTCCAGAGCTC 5
LOCUS	AU104331 Sugano Homo sapiens cDNA library EST 30-AUG-2001	LOCUS	AU104331 Sugano Homo sapiens cDNA library EST 30-AUG-2001
DEFINITION	COL0073, mRNA sequence.	DEFINITION	COL0073, mRNA sequence.
ACCESSION	AU104331	ACCESSION	AU104331
VERSION	EST	VERSION	EST
KEYWORDS	Homo sapiens (human)	KEYWORDS	Homo sapiens (human)
SOURCE	Organism: Buteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 50)	SOURCE	Organism: Buteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 50)
REFERENCE	Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.	REFERENCE	Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
AUTHORS	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites	AUTHORS	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
TITLE	EMBO Rep. 2 (5), 388-393 (2001)	TITLE	EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)	JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE	21270072	MEDLINE	21270072
PUBLISHED	11375929	PUBLISHED	11375929
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-6539, Japan Email: yasuzuki@ims.u-tokyo.ac.jp Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).	COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-6539, Japan Email: yasuzuki@ims.u-tokyo.ac.jp Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES source	1. 50 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="COL0073" /clone_lib="Sugano Homo sapiens cDNA library"	FEATURES source	Location/Qualifiers
ORIGIN	Query Match Best Local Similarity 2.9%; Score 19.8; DB 9; Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	ORIGIN	Query Match Best Local Similarity 2.9%; Score 19.8; DB 9; Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 629 AGATGGAGAACTGGAGAGAAGTGTGAGC 659 LOCUS BI669410 mRNA linear EST 12-SEP-2001
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 20 AGATGGAGAACTGGAGAGAAGTGTGAGC 50 LOCUS BI669410.1 GI:15583643
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 7

LOCUS AL757838/c DNA linear GSS 18-JUN-2002
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-152H09-013139,
Genomic survey sequence.
ACCESSION AL757838
VERSION GI:21496186
KEYWORDS GSS
SOURCE Organism: Homo sapiens (human)
Organism: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
COMMENT
Email: cgdbs-f@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
National Institutes of Health, Mammalian Gene Collection (MGCC)
NIH-MGCC http://mgc.ncbi.nlm.nih.gov/
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgdbs-f@mail.nih.gov
Tissue Procurement: Michael J. Brownstein (NHGR), Shiraki
CDNA Library Preparation: Toshiyuki and Piero Carninci (IREN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM11797 Row: m Column: 23
High quality sequence stop: 41.

1. 41
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="axon:9606"
/clone="IMAGE:5314750"
/tissue type="hypothalamus"
/lab_host="IDH10B"
/clone_id="NIH_MGC_96"
/note="Organ: Brain; Vector: pBluescript (modified
pBluescript KS+); Site: BamHI; Site 2: SalI-XbaI
tgtcgat"; Oligo-dT primed using primer
5'-TTTTTTTTTTTVA-3'; size selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

FEATURES Source
1. 41
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="axon:9606"
/clone="IMAGE:5314750"
/tissue type="hypothalamus"
/lab_host="IDH10B"
/clone_id="NIH_MGC_96"
/note="Organ: Brain; Vector: pBluescript (modified
pBluescript KS+); Site: BamHI; Site 2: SalI-XbaI
tgtcgat"; Oligo-dT primed using primer
5'-TTTTTTTTTTTVA-3'; size selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

REFERENCE
AUTHORS Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
TITLE A Pipeline for automated high-throughput generation of ESTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
JOURNAL Unpublished
2.
REFERENCE
AUTHORS Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K., and Weisshaar, B.
TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
JOURNAL Unpublished
3. (bases 1 to 47)
REFERENCE Strizhov, N., Li, Y., Rosso, M., and Weisshaar, B.
TITLE Direct Submission
SUBMITTED (17-10-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene At4g18700. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpi-zkoeln.mpg.de/GABI-Kat/
FEATURES Location/Qualifiers
1. 47
/organism="Arabidopsis thaliana"
/mol_type="Genomic DNA"
/strain="Columbia 0"
/db_xref="axon:3702"
/clone_id="GK-152H09-013139"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC51. The lines contain one or more T-DNA
insertions. The DNA fragment (s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"

ORIGIN
LOCUS BI544737/c mRNA linear EST 05-SEP-2001
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Query Match 2.9% Score 19.4; DB 12; Length 41;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 8

Query Match 2.9% Score 19.6; DB 29; Length 47;
Best Local Similarity 73.5%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 9

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 10

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 11

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 12

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 13

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 14

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 15

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 16

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 17

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 18

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 19

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 20

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 21

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 22

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 23

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 24

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 25

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 26

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 27

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 28

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 29

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 30

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 31

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 32

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 33

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 34

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 35

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 36

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 37

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 38

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 39

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 40

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 41

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 42

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 43

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

RESULT 44

Query Match 2.9% Score 19.4; DB 12; Length 47;
Best Local Similarity 79.3%; Pred. No. 1.1e+06; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 571 GAGGTGCCATTAGCCTAAATTCTAGGAGTCGGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.
mRNA sequence.

Db 39 GAGATCCCATAGTTGGAGTCGGCTCCGCT 604 LOCUS BI544737/1 GI:15432049
mRNA sequence.
mRNA sequence.
mRNA sequence.

Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 DNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
 DNA Sequencing by: Incyte Genomics Inc.
 Clone distribution: MGCI clone distribution information can be
 found through the I.M.A.G.E. Consortium/LILNL at:
<http://image.llnl.gov>
 Plate: LILNL19 Row: A column: 01
 High quality sequence stop: 47.

FEATURES
 source
 1. 47
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="KAT03974"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match	Match	Score	DB	Length
Qy	258	2.9%	19.4	50;
Db	37	2.9%	19.4	50;

RESULTS 11

LOCUS	DEFINITION	OP	EST
BG314884	Human THP1 cell line library Homo sapiens cDNA, mRNA sequence.	0.138	
BG314884	GI:18997731	0.1	
BG314884	EST.		
Homo sapiens (human)	ORGANISM		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo	REFERENCE		
Odeberg,J.; Andersson,T.; Borring,S.; Larsson,M.; Thelin,A.; Ekstrand-Hammarstrom,B.; Wirta,V.; Wenborg,A.; Lundberg,J. and	AUTHORS	1 ('bass 1 to 50) Unpublished (2001)	
Identification of candidate genes in atherosclerosis - Virtual chip analysis in RDA based transcript profiling of monocyte/macrophage	TITLE		
KTH Teknikringen 34, plan 6, 100 44 Stockholm, Sweden	JOURNAL		
Tel: +46 8 790 71 29 Fax: +46 8 245452	COMMENT		

RESULTS 12

LOCUS	DEFINITION	OP	EST	
AU106356	Sugano Homo sapiens cDNA library Homo sapiens mRNA sequence.	0.13e+06		
AU106356	GI:135555177	1		
Homo sapiens (human)	ORGANISM			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE			
(bases 1 to 50)	AUTHORS			
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ob,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Sugano,A. and Sugano,S.	TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)		
JOURNAL	Match	Score	DB	Length
PUBMED	21270072	2.9%	19.4	50;
COMMENT	11375929	68.4%	1.3e+06	

RESULTS 13

LOCUS	DEFINITION	OP	EST
AU104702	Sugano Homo sapiens cDNA library Homo sapiens mRNA sequence.	0.13e+06	
AU104702	GI:170 GGGCCCTGCATGGAAAGACTGCAGAGAAGCTGTGGAG 207	1	
HRC06060	7 GAGCGTGTGGTAGGACGGAGTGAAGCTGGNAG 44	0	

RESULTS 14

LOCUS	DEFINITION	OP	EST
AU104702	Sugano Homo sapiens cDNA library Homo sapiens mRNA sequence.	0.13e+06	
HRC06060	50 bp mRNA linear Homo sapiens cDNA library	1	

The P element insertion position is base 035 in the 42 bases. This insertion position refers to the first base of the 8 base target recognition sequence.

ORGANISM *Homo sapiens* (human)

KEYWORDS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates;

REFERENCE Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Ota, T., Iegai, Y., Tanaka, T., Morishita, S., Okubo, K., Sakai, Y., Nakamura, Y., Sugano, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 11375929

PUBLMED

COMMENT Contact: Yutaka Suzuki
Institute of Medical Science, University of Tokyo
4-6-1, Shin Okandai, Minato-ku, Tokyo 108-8339, Japan
Email: yuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Sugano, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES source

1. .50 /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="HR06050"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match Score 19.2; DB 9; Length 50;
Best Local Similarity 2.9%; Pred. No. 1.5e+06;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 244 CNGGCCCTGCTGGGGCACACACCCCTGCTCAGC 283
Db 11 CTGGCCGCCAGGGGGCCAGCCAGGCCGTGC 50

RESULT 13 AQ025866/C

DEFINITION 1(2)8708 Drosophila melanogaster P lethal line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.

VERSION AQ025866_1

KEYWORDS Drosophila melanogaster (fruit fly)

ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Sphyradoidea; Drosophilidae; Drosophilidae;

REFERENCE Spradling, A.C., Stern, D., Beaton, A., Rehm, B.J., Laverty, T., Mozena, N., Misra, S. and Rubin, G.M.

TITLE The BDGP Gene disruption Project: Single P element insertions mutating 30% of Drosophila autosomal genes

JOURNAL Unpublished (1999)

COMMENT Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
USA Building, Berkeley, CA 94720-3200, USA
Fax: 5106339947
Email: gerry@fruitfly.berkeley.edu

Sequence orientation is forward strand relative to 5' end of P element

The P element insertion position is base 035 in the 42 bases. This insertion position refers to the first base of the 8 base target recognition sequence.

FEATURES source

1. .42 /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_xref="taxon:7227"
/clone lib="Drosophila melanogaster P lethal line"
/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains a single P transposable element insertion that is thought to cause either lethality or sterility. The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/P disrupt/inverse_pcr.html. "

ORIGIN

Query Match Score 19; DB 28; Length 42;
Best Local Similarity 2.8%; Pred. No. 1.5e+06;
Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 21 AGCTCATACTGCAACCATCCCGCTGACAGTCACAG 56
Db 36 AGTACTATAATGGCTCATNCCCCATCCGGCCAG 1

RESULT 14 AZ479659/C

LOCUS IM0300B03R Mouse 10rb plasmid UGCLM library Mus musculus genomic clone UGCLM0300B03 R, genomic survey sequence.

DEFINITION AZ479659

ACCESSION AZ479659.1

VERSION GI:10639488

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 50)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meinen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederauern, A. and Wright, D., Weiss, R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

FEATURES source

1. .50 /organism="Mus musculus"
/mol type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0300B03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tr-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"

/note="Vector: PWD42mv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnarefs/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA Polymerase and T4 Polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD2 (G1473114 9kb [AT12907.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insect adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL1-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

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Matches 28; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 548 CAGATGGTGTCTGACCCGTTCAAGGTGCCATTAGCAATT 590
Db 49 CAGITGGTGTCTCAGGCAATTAAACACTCCATTACCAATT 7

RESULT 15

AU106353/C AU106353 Sugano Homo sapiens 50 bp mRNA linear EST 30-AUG-2001
DEFINITION COLO0742, mRNA sequence.
ACCESSION AU106353
VERSION AU106353.1 GI:13555874
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Shizuka,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
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Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full-length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES Location/Qualifiers
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organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 2.8%; Score 18.8; DB 9; Length 50;
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Matches 26; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 264 CACACACACCCCTGCTCAGGAGGTCTCCGGCTCGGCC 301
Db 49 CCCAGGACAAAGAACCTCCGGCTCAAGCGGCC 1.2

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Job time : 2036.49 secs